

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:46:27 ; Search time 2853.47 Seconds
(without alignments)
295.138 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18

Sequence: 1 cggatgtctatttga 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 106998

Minimum DB seq length: 0

Maximum DB seq length: 4033

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_ges1:*

10: gb_ges2:*

11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.4	68.9	24	9	AZ846667 2M0146P24
2	12.4	68.9	34	1	AU258674 AU258674
3	12.4	68.9	37	9	BZ287861 SALK 0212
4	12.4	68.9	40	9	AZ822722 2M0096008
5	11.8	65.6	20	10	CL313440 mth2-128N
6	11.8	65.6	30	10	CZ469644 c04964-5p
7	11.8	65.6	37	10	CZ477101 d10098-3p
8	11.6	64.4	29	10	AB081925 Drosophila
9	11.6	64.4	30	10	CZ487985 f05420-3p
10	11.4	63.3	21	9	AZ402083 1M0169A15
11	11.4	63.3	28	9	AZ471813 1M0286D06
12	11.4	63.3	31	10	AG192945 Pan trogl
13	11.4	63.3	36	6	CA851372 D13A08 A0
14	11.2	62.2	24	10	AJ587601 Arabidops
15	11.2	62.2	27	9	BZ768666 SALK 1405
16	11.2	62.2	28	1	AI690628 tx98g09.x
17	11.2	62.2	30	10	CZ470021 c05477b-5
18	11.2	62.2	34	1	AV852639 AV852639
19	11	61.1	37	10	CZ489987 f07187-5p
20	11	61.1	39	1	AU006827 AU006827
21	10.8	60.0	27	9	AZ478637 1M0298B23
22	10.8	60.0	29	9	AZ803680 2M0064009

23	10.8	60.0	31	1	AU009970
24	10.8	60.0	31	1	AU009989
25	10.8	60.0	31	10	BX532321 Arabidops
26	10.8	60.0	31	10	BX532876 Arabidops
c 27	10.8	60.0	32	6	CA851642 D16A01 B1
c 28	10.8	60.0	33	1	AV836794 AV836794
29	10.8	60.0	33	8	D11586 HUM0C12H05
30	10.8	60.0	34	8	D11855 HUM0C12H05
31	10.8	60.0	34	8	N30120 YW63H05.s1
32	10.8	60.0	34	10	BX661869 Arabidops
33	10.8	60.0	36	9	AZ398982 1M0164D08
c 34	10.8	60.0	36	9	AZ767524 1M0566E15
35	10.8	60.0	36	10	CZ551808 CB2 1687
36	10.8	60.0	36	10	CZ919151 4021012A0
c 37	10.8	60.0	36	10	AL944589 Arabidops
c 38	10.8	60.0	37	1	AI016852 ou27b03.x
39	10.8	60.0	37	10	AL944588 Arabidops
40	10.8	60.0	38	10	CZ559623 PL00353-5
41	10.8	60.0	40	10	BX536158 Arabidops
c 42	10.6	58.9	24	9	AZ763574 1M0559P01
c 43	10.6	58.9	25	9	AZ768828 1M0569C06
44	10.6	58.9	25	10	CZ467409 c01749-3p
c 45	10.6	58.9	25	10	CZ483624 f01137-3p

ALIGNMENTS

RESULT 1

AZ846667

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AZ846667 24 bp DNA linear GSS 21-FEB-2001
2M0146P24R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0146P24 R, genomic survey sequence.

AZ846667
A2846667.1 GI:13027929

GSS.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00
Plate: 0146 row: P column: 24
Seq primer: CACACGAAACACCTAIGACC
Class: plasmid ends

High quality sequence stop: 24.
Location/Qualifiers
1. 24

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0146P24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor to the insert adaptors and adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGATGCTATTGTTT 15
|||||
Db 7 GGCGATGCTATTGTTT 20

RESULT 2

AU258674

LOCUS

DEFINITION AU258674 3'-directed mouse cDNA library Mus musculus cDNA clone

BED0013458 3', mRNA sequence.

ACCESSION AU258674

VERSION AU258674.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 34)

Kato, K. and Matoba, R.

Generation of expressed sequence tags from mouse brain

Unpublished (2002)

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkato@bs.nist-nara.ac.jp

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

source

1..34
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0013458"
/tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN

Query Match 68.9%; Score 12.4; DB 1; Length 34;
Best Local Similarity 92.9%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ATGTCATTGTTGTA 18

|||||

20 ATGTCATTGTTGAA 33

RESULT 3

BZ287861

LOCUS

DEFINITION BZ287861 37 bp DNA linear GSS 24-OCT-2002
SALK_021239.53.05.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_021239.53.05.x, genomic
survey sequence.

ACCESSION

BZ287861

VERSION

BZ287861.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 37)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of

At1g08980.

Class: TDNA tagged.

Location/Qualifiers

1..37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_021239.53.05.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 68.9%; Score 12.4; DB 9; Length 37;

Best Local Similarity 92.9%; Pred. No. 1.8e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTATTGTTG 16

|||||

Db 22 GCATATCTATTGTTG 35

RESULT 4

AZ822722

LOCUS

DEFINITION

AZ822722

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0096 row: 0 column: 08
 Seq primer: CGTGTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 40.

FEATURES
 source
 1..40
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M096008"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGIM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (Gill4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 68.9%; Score 12.4; DB 9; Length 40;
 Best Local Similarity 92.9%; Pred. No. 1.8e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGCTCTATTGTTGT 17
 |||||
Db 5 CATGCTCTACTTGT 18

RESULT 5
CL313440/c
LOCUS
DEFINITION mch2-128N01_OP Medicago truncatula BAC end sequences Medicago truncatula genomic 5', genomic survey sequence.
ACCESSION CL313440.1 GI:44831114
VERSION GSS.
KEYWORDS Medicago truncatula (barrel medic)
SOURCE Medicago truncatula
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 20)

AUTHORS Jakab, J., Deak, G., Kevei, Z., Karchesz, K., Sarai, E., Kiss, P., Kereszt, A., Kalo, P., Endre, G. and Kiss, G.B.
TITLE Medicago Truncatula BAC end sequencing
JOURNAL Unpublished (2004)
COMMENT Contact: Deak, G.
 Alfalfa Genomics Group; Medicago Genetics Group
 Agricultural Biotechnology Center; Biological Research Center
 P.O. Box 411, Hungary, H-2100 Godollo, Szent-Gyorgyi Albert ut 4.;
 P.O. BOX 521, Hungary, H-6701 Szeged, Temesvari krt. 62
 Tel: 3628526142
 Fax: 3628526193
 Email: gdeak@abc.hu
 Plate: 128 row: N column: 01
 Seq primer: OP Reverse
 Class: BAC ends.

FEATURES
 Location/Qualifiers
 1..20
 /organism="Medicago truncatula"
 /mol_type="genomic DNA"
 /cultivar="Jemalong"
 /isolate="A17"
 /db_xref="taxon:3880"
 /sex="Hermaphrodite"
 /clone_lib="Medicago truncatula BAC end sequences"
 /note="Organ: Leaf; Vector: pBeloll; Site: 1: HindIII; Site 2: HindIII; Construction of a bacterial artificial chromosome library of Medicago truncatula and identification of clones containing ethylene-response genes. Theor Appl Genet (1999) 98: 638-646 Y.-W. Nam; R.V. Pennetsa; G. Endre; P. Uribe; D. Kim; D.R. Cook"

ORIGIN
 Query Match 65.6%; Score 11.8; DB 10; Length 20;
 Best Local Similarity 81.2%; Pred. No. 3.6e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCAGTCTCTATTGTTG 16
 |||||
Db 16 CGCAGTCTTTTGTG 1

RESULT 6
LOCUS CZ469644
DEFINITION c04964-Sprime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac, genomic survey sequence.
ACCESSION CZ469644
VERSION CZ469644.1 GI:62963657
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 30)
 Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartout, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Lauffer, A., Mazotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
 A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac
 Nat. Genet. 36 (3), 283-287 (2004)
 Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798

Email: RHoskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of piggyBac element.
 The piggyBac insertion position is 27 in the 30 bases. This insertion position refers to the first base of the 4 base TTA target recognition sequence.
 Class: transposon insertion site.
 Location/Qualifiers
 1..30
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis PB insertions"
 /note="Vector: piggyBac PB (GenBank accession number AY15146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

FEATURES

source

1..30
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis piggyBac PB insertions"
 /note="Vector: piggyBac PB (GenBank accession number AY15146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 65.6%; Score 11.8; DB 10; Length 30;
 Best Local Similarity 86.7%; Pred. No. 3.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTTTGT 17
 Db 12 GCATGCTCTATTTT 26

RESULT 7

CZ477101/c
 LOCUS
 DEFINITION 37 bp DNA linear GSS 29-APR-2005
 d10098-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

ACCESSION CZ477101

VERSION CZ477101.1 GI:62972138

SOURCE GSS.

ORGANISM Drosophila melanogaster (fruit fly)

REFERENCE Drosophila melanogaster

AUTHORS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 37)

Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,

Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,

Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,

Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,

Lauffer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,

Swimmer,C., Kopyzynski,C., Duyk,G., Winberg,M.L. and Margolis,J.

A complementary transposon tool kit for Drosophila melanogaster

using P and piggyBac

Nat. Genet. 36 (3), 283-287 (2004)

14981521

CONTACT: Roger A Hoskins

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA

Tel: 510 486 4015

Fax: 510 486 6798
 Email: RHoskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of P element.
 The P element insertion position is 1 in the 37 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
 Class: transposon insertion site.
 Location/Qualifiers
 1..37
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis P element XP insertions"
 /note="Vector: P element XP (GenBank accession number AY15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinacy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

FEATURES

source

1..37
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"
 /clone_lib="Exelixis P element XP insertions"
 /note="Vector: P element XP (GenBank accession number AY15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinacy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 65.6%; Score 11.8; DB 10; Length 37;
 Best Local Similarity 86.7%; Pred. No. 3.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCATGCTCTATTTT 15
 Db 29 CTGCATGCTCTCTTTT 15

RESULT 8

AB081925/c

LOCUS

DEFINITION 29 bp DNA linear GSS 25-FEB-2003

AB081925

AB081925.1 GI:21623935

GSS.

ORGANISM Drosophila melanogaster (fruit fly)

REFERENCE Drosophila melanogaster

AUTHORS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1

Oh,S.W., Kingsley,T., Shin,H.H., Zheng,Z., Chen,H.W., Chen,X.,

Wang,H., Ruan,P., Moody,M. and Hou,S.X.

A p-element insertion screen identified mutations in 455 novel

essential genes in Drosophila

Genetics 163 (1), 195-201 (2003)

12586707

2 (bases 1 to 29)

Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.

Direct Submission

Submitted (21-MAR-2002) Suwan Oh, The Laboratory of Immunobiology,

National Institutes of Health, National Cancer Institute,

Frederick, 1050 Boyles St., Frederick, Maryland 21702-1201, USA

(E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,

Fax:1-301-846-6145)

FEATURES

source

1..29

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="1(2)SH2 0218"

ORIGIN

Query Match 64.4%; Score 11.6; DB 10; Length 29;
 Best Local Similarity 77.8%; Pred. No. 4.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTGTGA 18
 |||||
 DB 29 CAGCAGTCTAAATTGAA 12

RESULT 9
 C2487985/c
 LOCUS
 DEFINITION f05420-3prime Exelixis piggyBac WH insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.

ACCESSION C2487985
 VERSION C2487985.1 GI:62985423
 KEYWORDS GSS.

ORGANISM Drosophila melanogaster (fruit fly)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Kopyzynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
 TITLE A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac

JOURNAL Nat. Genet. 36 (3), 283-287 (2004)
 PUBMED 14981521

COMMENT Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798

Email: Rhoskins@lbl.gov

Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of piggyBac element.
 The piggyBac insertion position is 1 in the 30 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.
 Class: transposon insertion site.

FEATURES
 source

1..30
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="isogenic w- strain"
 /db_xref="taxon:7227"

/clone_lib="Exelixis piggyBac WH insertions"
 /note="Vector: piggyBac WH (GenBank accession number AF151148); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the WH element using the constitutive alpha-1 tubulin:piggyBac transposase source. We remobilized the WH element from a single ammunition element on the Binsincy balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 64.4%; Score 11.6; DB 10; Length 30;

Best Local Similarity 77.8%; Pred. No. 4.5e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTGTGA 18
 |||||
 DB 19 CGGCTTTCTTTTTTTA 2

RESULT 10
 AZ402083

LOCUS
 DEFINITION

ACCESSION AZ402083

VERSION AZ402083.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0169 row: A column: 15

Seq primer: CGTTGTAACAGCGGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUCIM0169A15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.3%; Score 11.4; DB 9; Length 21;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTATTGTTT 15
 |||||
 Db 4 GCATTTCTATTGTTT 16
 |||||

RESULT 11
 AZ471813/c
 LOCUS
 DEFINITION IM0286D06R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0286D06 R, genomic survey sequence.

ACCESSION AZ471813
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0286 row: D column: 06
 Seq primer: CACACAGGAACACGTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES
 source
 1. 28
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0286D06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.3%; Score 11.4; DB 9; Length 28;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CATGCTATTGTTG 16
 |||||
 Db 14 CATGGCTATTGTTG 2
 |||||

RESULT 12
 AG192945
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: RP43-069M06.T7, genomic survey sequence.

ACCESSION AG192945
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Pan troglodytes (chimpanzee)
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pan.

REFERENCE 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Run, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 TITLE BAC end sequences of Library RP-43
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 31)
 TITLE Direct Submission
 JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC); S2, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea (E-mail:redaction@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
 COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI
 Location/Qualifiers
 1. 31
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-069M06.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
 Query Match 63.3%; Score 11.4; DB 10; Length 31;
 Best Local Similarity 92.3%; Pred. No. 5.7e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TGTCTATTGTTGTA 18
 |||||
 Db 17 TGTCTATTGTTGTA 29
 |||||

RESULT 13
 CA851372/c
 LOCUS
 DEFINITION D13A08 A08.02.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D13A08 5', mRNA sequence.

ACCESSION CA851372
 VERSION CA851372.1 GI:33388165

KEYWORDS
SOURCE EST.
ORGANISM Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 36)
AUTHORS Alkharouf, N., Khan, R. and Matthews, B.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Genome 47 (2), 380-388 (2004)
PUBMED 15060591
COMMENT Contact: Alkharouf, N.W.
 Soybean Genomics and Improvement Laboratory (SGIL)
 US Department of Agriculture (USDA), ARS, PSI
 Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
 Tel: 301 504 5750
 Fax: 301 504 5728
 Email: alkharouf@ba.ars.usda.gov.
FEATURES
 source
 1..36
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Peking"
 /db_xref="taxon:3847"
 /clone="D13A08"
 /tissue_type="Roots"
 /dev_stage="Seedlings"
 /clone_lib="cDNA Peking library 2, 4 day SCN3"
 /note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
ORIGIN
 Query Match 63.3%; Score 11.4; DB 6; Length 36;
 Best Local Similarity 80.0%; Pred. No. 5.8e+05;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 CATGCTATTGTGTA 18
 || |||||
 Db 15 CANNCTATTTTTA 1
RESULT 14
 AJ587601 24 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 298H08, genomic survey sequence.
DEFINITION Arabidopsis thaliana T-DNA flanking sequence.
ACCESSION AJ587601.1 GI:37937225
VERSION AJ587601.1
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 24)
AUTHORS Balzergue, S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
FEATURES
 source
 1..24
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="298H08"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 1..24
 /note="T-DNA flanking sequence left border"
misc_feature
 1..24
 /note="T-DNA flanking sequence left border"
ORIGIN
 Query Match 62.2%; Score 11.2; DB 10; Length 24;
 Best Local Similarity 81.2%; Pred. No. 7.2e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 GGCATGCTATTGTGTTGT 17
 ||| |||||
 Db 1 GGCCTGTGTAATTGTTGT 16
RESULT 15
 BZ768666/c 27 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_140548.46.70.x Arabidopsis thaliana T-DNA insertion lines Arabidopsis thaliana genomic clone SALK_140548.46.70.x, genomic survey sequence.
DEFINITION Arabidopsis thaliana genomic clone SALK_140548.46.70.x, genomic survey sequence.
ACCESSION BZ768666.1 GI:28942307
VERSION BZ768666
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 27)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of T-DNA.
Class: T-DNA tagged.
Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_140548.46.70.x"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 62.2%; Score 11.2; DB 9; Length 27;
Best Local Similarity 81.2%; Pred. No. 7.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGTGA 18
|||
Db 26 GCTTGTCTCTTTTGA 11

Search completed: March 4, 2006, 03:39:01
Job time : 2857.47 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:48 ; Search time 375.632 Seconds
(without alignments)
396.263 Million cell updates/sec

Title: US-09-701-583A-9
Perfect score: 18
Sequence: 1 cggcatgtctatttga 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10900902

Minimum DB seq length: 0

MaximumDB:seqlength=406

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	5	US-10-146-058-72
2	18	100.0	18	6	US-10-220-033-4
3	18	100.0	18	9	US-10-984-919-1209
4	16	88.9	16	9	US-10-984-919-1277
5	16	88.9	20	6	US-10-189-267-40
6	16	88.9	20	6	US-10-189-267-185
7	16	88.9	20	9	US-10-984-919-529
8	14.8	82.2	20	6	US-10-189-267-116
9	14.8	82.2	20	6	US-10-189-267-243
10	14.8	82.2	25	5	US-10-098-263B-91037
11	14.8	82.2	25	10	US-11-036-317-121656
12	14.8	82.2	25	10	US-11-060-756-190386
13	14.8	82.2	25	10	US-11-060-756-259860
14	14.4	80.0	25	8	US-10-719-900-86562
15	14.4	80.0	25	10	US-11-036-317-194446
16	14.4	80.0	25	10	US-11-036-317-253543
17	14.4	80.0	25	10	US-11-036-317-276997
18	14.4	80.0	25	10	US-11-036-317-310713
19	14.4	80.0	25	10	US-11-036-317-334637
20	14.4	80.0	25	10	US-11-036-317-383155
21	14	77.8	20	6	US-10-189-267-54
22	14	77.8	20	6	US-10-189-267-197
23	14	77.8	25	10	US-11-036-317-474175

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c 24      14      77.8      25 10 US-11-036-317-777184
c 25      13.8      76.7      25 7 US-10-719-956-180828
c 26      13.8      76.7      25 7 US-10-719-956-583979
c 27      13.8      76.7      25 8 US-10-719-900-715769
c 28      13.8      76.7      25 10 US-11-036-317-198172
c 29      13.8      76.7      25 10 US-11-036-317-229607
c 30      13.8      76.7      25 10 US-11-036-317-239950
c 31      13.8      76.7      25 10 US-11-036-317-294363
c 32      13.8      76.7      25 10 US-11-036-317-322759
c 33      13.8      76.7      25 10 US-11-036-317-439359
c 34      13.4      74.4      20 6 US-10-053-662A-7
c 35      13.4      74.4      25 5 US-10-098-263B-55957
c 36      13.4      74.4      25 7 US-10-719-956-518120
c 37      13.4      74.4      25 8 US-10-719-900-60048
c 38      13.4      74.4      25 8 US-10-719-900-589217
c 39      13.4      74.4      25 8 US-10-719-900-592572
c 40      13.4      74.4      25 8 US-10-719-900-808618
c 41      13.4      74.4      25 9 US-10-956-157-51384
c 42      13.4      74.4      25 9 US-10-956-157-51387
c 43      13.4      74.4      25 9 US-10-956-157-51389
c 44      13.4      74.4      25 9 US-10-956-157-51390
c 45      13.4      74.4      25 9 US-10-956-157-271471

```

ALIGNMENTS

```

RESULT 1
US-10-146-058-72
; Sequence 72, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 72:

```

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
US-10-146-058-72

Query Match      100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 2
US-10-220-033-4
/ Sequence 4, Application US/10220033
/ Publication No. US20030186906A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlingensiepen, Karl-Hermann
/ TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
/ TITLE OF INVENTION: and a molecule binding to an expression product of that
/ TITLE OF INVENTION: gene
/ FILE REFERENCE: P68119US0
/ CURRENT APPLICATION NUMBER: US/10/220,033
/ CURRENT FILING DATE: 2003-03-17
/ PRIOR APPLICATION NUMBER: PCT/EP01/02694
/ PRIOR FILING DATE: 2001-03-10
/ PRIOR APPLICATION NUMBER: EP00105190.3
/ PRIOR FILING DATE: 2000-03-11
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: antisense
/ OTHER INFORMATION: oligonucleotide
US-10-220-033-4

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 3
US-10-984-919-1209
/ Sequence 1209, Application US/10984919
/ Publication No. US20050130927A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlingensiepen, Karl-Hermann
/ TITLE OF INVENTION: Antisense oligonucleotide preparation method
/ FILE REFERENCE: 10496/P63763US0
/ CURRENT APPLICATION NUMBER: US/10/984,919
/ CURRENT FILING DATE: 2004-11-10
/ PRIOR APPLICATION NUMBER: US/09/341,700
/ PRIOR FILING DATE: 1999-09-24
/ PRIOR APPLICATION NUMBER: PCT/EP98/00497
/ PRIOR FILING DATE: 1998-01-30
/ PRIOR APPLICATION NUMBER: EP 97 101 531.8
/ PRIOR FILING DATE: 1997-01-31
/ NUMBER OF SEQ ID NOS: 1764
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: antisense
/ OTHER INFORMATION: oligonucleotide
US-10-984-919-1209

Query Match      100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 4
US-10-984-919-1277
/ Sequence 1277, Application US/10984919
/ Publication No. US20050130927A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlingensiepen, Karl-Hermann
/ TITLE OF INVENTION: Antisense oligonucleotide preparation method
/ FILE REFERENCE: 10496/P63763US0
/ CURRENT APPLICATION NUMBER: US/10/984,919
/ CURRENT FILING DATE: 2004-11-10
/ PRIOR APPLICATION NUMBER: US/09/341,700
/ PRIOR FILING DATE: 1999-09-24
/ PRIOR APPLICATION NUMBER: PCT/EP98/00497
/ PRIOR FILING DATE: 1998-01-30
/ PRIOR APPLICATION NUMBER: EP 97 101 531.8
/ PRIOR FILING DATE: 1997-01-31
/ NUMBER OF SEQ ID NOS: 1764
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1277
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1277

Query Match      88.9%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTG 16
Db 1 CGGCATGCTCTATTGTG 16

RESULT 5
US-10-189-267-40
/ Sequence 40, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189,267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 40
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
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/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1209
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1209

Query Match      100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 4
US-10-984-919-1277
/ Sequence 1277, Application US/10984919
/ Publication No. US20050130927A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlingensiepen, Karl-Hermann
/ TITLE OF INVENTION: Antisense oligonucleotide preparation method
/ FILE REFERENCE: 10496/P63763US0
/ CURRENT APPLICATION NUMBER: US/10/984,919
/ CURRENT FILING DATE: 2004-11-10
/ PRIOR APPLICATION NUMBER: US/09/341,700
/ PRIOR FILING DATE: 1999-09-24
/ PRIOR APPLICATION NUMBER: PCT/EP98/00497
/ PRIOR FILING DATE: 1998-01-30
/ PRIOR APPLICATION NUMBER: EP 97 101 531.8
/ PRIOR FILING DATE: 1997-01-31
/ NUMBER OF SEQ ID NOS: 1764
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1277
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1277

Query Match      88.9%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTG 16
Db 1 CGGCATGCTCTATTGTG 16

RESULT 5
US-10-189-267-40
/ Sequence 40, Application US/10189267
/ Publication No. US20040006030A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Susan M. Freier
/ APPLICANT: Kenneth W. Dobie
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
/ FILE REFERENCE: PTS-0038
/ CURRENT APPLICATION NUMBER: US/10/189,267
/ CURRENT FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 284
/ SEQ ID NO 40
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-40

Query Match 88.9%; Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTG 16
Db 5 CGGCATGCTCTATTG 20

RESULT 6
US-10-189-267-185/c
; Sequence 185, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-185

Query Match 88.9%; Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTG 16
Db 16 CGGCATGCTCTATTG 1

RESULT 7
US-10-984-919-529
; Sequence 529, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-529

Query Match 88.9%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCATGCTATTGTA 18
Db 1 GCATGCTATTGTA 16

RESULT 8
US-10-189-267-116
; Sequence 116, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-116

Query Match 82.2%; Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTA 18
Db 1 CGGCATGCTCGATTGTA 18

RESULT 9
US-10-189-267-243/c
; Sequence 243, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-243

Query Match 82.2%; Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTA 18
Db 20 CGGCATGCTCGATTGTA 3

RESULT 10
US-10-098-263B-91037
; Sequence 91037, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1


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; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 194446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-194446

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Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      3 GCATGCTCTATTTCGTA 18
      |||||
Db      25 GCATGCTCTATTTCGTA 10

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Job time : 375.632 secs

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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:58:42 ; Search time 446.211 Seconds
(without alignments)
88.444 Million cell updates/sec

Title: US-09-701-583A-9
Perfect score: 18
Sequence: 1 cggcatgtctattttgta 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11581468

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
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4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
5: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	94.4	25	US-11-121-849-319164	Sequence 319164,
2	17	94.4	25	US-11-121-849-319625	Sequence 319625,
3	13.8	76.7	22	US-10-310-914A-461071	Sequence 461071,
4	13.8	76.7	22	US-10-310-914A-378741	Sequence 378741,
5	13.4	74.4	22	US-10-310-914A-1375953	Sequence 1375953,
6	13.4	74.4	25	US-11-121-849-151115	Sequence 151115,
7	13.4	74.4	25	US-11-136-527-153306	Sequence 153306,
8	13.4	74.4	25	US-11-136-527-153312	Sequence 153312,
9	13.4	74.4	25	US-11-136-527-153313	Sequence 153313,
10	13.4	74.4	25	US-11-136-527-153325	Sequence 153325,
11	13.4	74.4	25	US-11-136-527-153326	Sequence 153326,
12	13.4	74.4	25	US-11-136-527-153341	Sequence 153341,
13	13.4	74.4	25	US-11-121-849-245961	Sequence 245961,
14	13.2	73.3	25	US-11-101-244-1437211	Sequence 1437211,
15	13	72.2	19	US-11-101-244-1437212	Sequence 1437212,
16	13	72.2	19	US-11-101-244-1437218	Sequence 1437218,
17	13	72.2	19	US-11-083-784-1437211	Sequence 1437211,
18	13	72.2	19	US-11-083-784-1437212	Sequence 1437212,
19	13	72.2	19	US-11-083-784-1437218	Sequence 1437218,
20	13	72.2	19	US-11-083-784-1437218	Sequence 1437218,

c	21	13	72.2	23	8	US-10-310-914A-680711	Sequence 680711,
	22	13	72.2	24	8	US-10-310-914A-986600	Sequence 986600,
	23	13	72.2	25	12	US-11-121-849-108655	Sequence 108655,
c	24	12.8	71.1	18	8	US-10-310-914A-291549	Sequence 291549,
c	25	12.8	71.1	19	8	US-10-310-914A-1023769	Sequence 1023769,
	26	12.8	71.1	19	10	US-11-101-244-617220	Sequence 617220,
	27	12.8	71.1	19	10	US-11-101-244-617251	Sequence 617251,
	28	12.8	71.1	19	10	US-11-101-244-1125173	Sequence 1125173,
	29	12.8	71.1	19	11	US-11-083-784-617220	Sequence 617220,
	30	12.8	71.1	19	11	US-11-083-784-617251	Sequence 617251,
	31	12.8	71.1	19	11	US-11-083-784-1125173	Sequence 1125173,
c	32	12.8	71.1	20	8	US-10-310-914A-375180	Sequence 375180,
c	33	12.8	71.1	21	8	US-10-310-914A-289791	Sequence 289791,
	34	12.8	71.1	22	8	US-10-310-914A-476895	Sequence 476895,
c	35	12.8	71.1	22	8	US-10-310-914A-805261	Sequence 805261,
c	36	12.8	71.1	22	8	US-10-310-914A-805263	Sequence 805263,
c	37	12.8	71.1	23	8	US-10-310-914A-375181	Sequence 375181,
c	38	12.8	71.1	23	8	US-10-310-914A-805246	Sequence 805246,
c	39	12.8	71.1	23	8	US-10-310-914A-1023780	Sequence 1023780,
c	40	12.8	71.1	24	8	US-10-310-914A-553186	Sequence 553186,
	41	12.8	71.1	24	8	US-10-310-914A-1343860	Sequence 1343860,
	42	12.8	71.1	25	8	US-10-310-914A-564999	Sequence 564999,
	43	12.8	71.1	25	12	US-11-121-849-7342	Sequence 7342, Ap
	44	12.8	71.1	25	12	US-11-121-849-112895	Sequence 112895,
	45	12.8	71.1	25	12	US-11-121-849-150728	Sequence 150728,

ALIGNMENTS

RESULT 1

US-11-121-849-319164
; Sequence 319164, Application US/11121849
; Publication No. US2005027080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319164
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-319164

Query Match

Best Local Similarity 94.4%; Score 17; DB 12; Length 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCATGCTATTGTGA 18

Db 1 GGCATGCTATTGTGA 17

RESULT 2

US-11-121-849-319625
; Sequence 319625, Application US/11121849
; Publication No. US2005027080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-319625

Query Match 94.4%; Score 17; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGCATGCTCTATTGTGA 17

RESULT 3

US-10-310-914A-461071
; Sequence 461071, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 461071
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-461071

Query Match 76.7%; Score 13.8; DB 8; Length 22;
Best Local Similarity 47.1%; Pred. No. 8.5e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 6 GUCAUGUCUACUUGUA 22

RESULT 4

US-10-310-914A-378741/c
; Sequence 378741, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 378741
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-378741

Query Match 76.7%; Score 13.8; DB 8; Length 24;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 17 GGCATTTGTATTGTGA 1

RESULT 5

US-10-310-914A-1375953/c
; Sequence 1375953, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1375953
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1375953

Query Match 74.4%; Score 13.4; DB 8; Length 22;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTGTG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 22 GGCATGCTCTATTGTG 8

RESULT 6

US-11-121-849-151115
; Sequence 151115, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 151115
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-151115

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CATGCTAGTTGTGA 15

RESULT 7

US-11-136-527-153306
; Sequence 153306, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136.527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294


```
Query Match      74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 12
US-11-136-527-153326
; Sequence 153326, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-153326

Query Match          74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
Db 11 GCATGCTCTATTGT 25

RESULT 13
US-11-136-527-153341
; Sequence 153341, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153341
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-153341

Query Match          74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCATGCTCTATTGT 17
Db 5 GCATGCTCTATTGT 19

RESULT 14
US-11-121-849-245961
; Sequence 245961, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 245961
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-245961

Query Match          73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGCATGCTCTATTGTA 18
Db 5 CGCATGCTCTATTGTA 22

RESULT 15
US-11-101-244-1437211/c
; Sequence 1437211, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1437211
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1437211

Query Match          72.2%; Score 13; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCATGCTCTATTT 14
Db 14 GGCATGCTCTATTT 2

Search completed: March 4, 2006, 03:54:51
Job time : 447.711 secs
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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:38:40 ; Search time 350.053 Seconds

(without alignments)
342.704 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18

Sequence: 1 cggcgtctattttgta 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4598950

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	2	AAQ78423 TGF-beta
2	18	100.0	18	3	Aaz65449 Immunosp
3	18	100.0	18	4	Aad18718 Human oli
4	18	100.0	18	14	Aeb01186 TGF-beta
5	18	100.0	22	3	Aaz65511 Immunosp
6	18	100.0	27	5	Aaf82681 Human TGF
7	16	88.9	16	3	Aaz65472 Immunosp
8	16	88.9	20	2	Aav48940 TGF-beta2
9	16	88.9	20	3	Aaz65448 Immunosp
10	16	88.9	20	3	Aaz65509 Immunosp
11	16	88.9	20	12	ADI80184 Human tra
12	16	88.9	20	12	ADI80039 Human tra
13	16	88.9	20	14	AEB01185 TGF-beta
14	14.8	82.2	20	12	ADI80242 Mouse tra
15	14.8	82.2	20	12	ADI80115 Human tra
16	14.8	82.2	25	9	ACI91046 Human mic
17	14.4	80.0	17	2	AAZ3221 Integrin
18	14	77.8	17	2	AAZ3222 Integrin
19	14	77.8	20	12	ADI80053 Human tra

c	20	14	77.8	20	12	ADI80196	Adi80196 Human tra
	21	13.8	76.7	20	4	AAF59836	AAF59836 Human pro
	22	13.4	74.4	20	9	ADA74096	Ada74096 Equine la
	23	13.4	74.4	25	9	ACI55966	ACI55966 Human mic
c	24	13.4	74.4	30	14	AEI14421	AEI14421 Plant lip
	25	13.2	73.3	25	9	ACK13008	ACK13008 Human mic
	26	13.2	73.3	25	9	ACK13010	ACK13010 Human mic
	27	13.2	73.3	25	9	ACI91047	ACI91047 Human mic
	28	13	72.2	17	2	AAZ3223	AAZ3223 Integrin
	29	12.8	71.1	20	12	ADP20509	ADP20509 Transcrip
c	30	12.8	71.1	22	3	AAC69355	AAC69355 Human ABC
	31	12.4	68.9	20	12	ADM33186	Adm33186 Oligo SEQ
	32	12.4	68.9	32	14	ADY71468	Ady71468 Trichinel
	33	12.4	68.9	37	12	ADQ26421	Adq26421 Brevibact
	34	12.4	68.9	37	13	ADR88316	ADR88316 Brevibact
c	35	12.2	67.8	18	3	Aaz76976	Aaz76976 Human bia
	36	12.2	67.8	18	12	ADQ81512	Adq81512 Synthetic
	37	12.2	67.8	18	12	ADQ81489	Adq81489 Synthetic
	38	12.2	67.8	18	12	ADQ81564	Adq81564 DNA oligo
	39	12.2	67.8	20	2	AAQ95371	AAQ95371 Primer A
	40	12.2	67.8	20	3	AAK99134	AAK99134 20-mer He
c	41	12.2	67.8	20	12	ADJ85601	Adj85601 Nucleic a
	42	12.2	67.8	23	9	ACF05388	ACF05388 Rat tumou
c	43	12.2	67.8	23	10	ADC83807	Adc83807 Human pap
	44	12.2	67.8	23	10	ADP43680	Adp43680 HPV 16 de
c	45	12.2	67.8	24	2	AAQ48628	AAQ48628 TNF-alpha

ALIGNMENTS

RESULT 1

AAQ78423

ID AAQ78423 standard; DNA; 18 BP.

XX AC AAQ78423;

XX DT 25-MAR-2003 (revised)

DT 27-JUN-1995 (first entry)

XX TGF-beta gene phosphorothioate antisense oligonucleotide.

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;

KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;

KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;

KW immunosuppression; oligonucleotide; ss.

XX OS Synthetic.

XX PN WO9425588-A2.

XX PD 10-NOV-1994.

XX PF 29-APR-1994; 94WO-EP001362.

XX PR 30-APR-1993; 93EP-00107089.

XX PR 13-MAY-1993; 93EP-00107849.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;

XX PI Bogdahn U;

XX DR WPI; 1994-358266/44.

XX PT New transforming growth factor beta anti-sense oligo:nucleotide(s) - for

XX PT treating immunosuppression, tumours, etc.

XX PS Claim 6; Page 44; 74pp; English.

XX CC The antisense oligonucleotides are useful in the treatment of tumours in

XX CC which expression of TGF-beta is of relevance for pathogenicity and/or

XX CC inhibition of pathological angiogenesis. They are used especially for the

CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTATTATTGTA 18
 |||||
 Db 1 CGGCATGCTATTATTGTA 18

RESULT 2

AAZ65449
 ID AAZ65449 standard; DNA; 18 BP.

XX
 AC AAZ65449;

XX
 DT 30-MAR-2000 (first entry)

XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-9.

XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX
 OS Unidentified.

XX
 PN WO9963975-A2.

XX
 PD 16-DEC-1999.

XX
 PF 10-JUN-1999; 99WO-BP004013.

XX
 PR 10-JUN-1998; 98EP-00110709.

XX
 PR 25-JUL-1998; 98EP-00113974.

XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;

XX
 DR WPI; 2000-097470/08.

XX
 PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX
 PS Claim 5; Fig 1; 30pp; English.

XX
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,

CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGF-beta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX
 SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTATTATTGTA 18

|||||
 Db 1 CGGCATGCTATTATTGTA 18

RESULT 3

AAAD18718

ID AAAD18718 standard; DNA; 18 BP.

XX
 AC AAAD18718;

XX
 DT 18-DEC-2001 (first entry)

XX
 DE Human oligonucleotide #4, useful in drug target validation.

XX
 KW Human; TGF-beta; erbB-2; MIA; c-jun; junB; c-fos; VCAM; NF-kappaB p65;
 KW NF-kappaB p50; ICAM; VEGF; NF-kB 2; therapy; tumour; immune disorder;
 KW organ transplantation; cell expansion; drug target validation;
 KW antitumour; immunosuppressive; ss.

XX
 OS Homo sapiens.

XX
 PN EP1133988-A1.

XX
 PD 19-SEP-2001.

XX
 PF 11-MAR-2000; 2000EP-00105190.

XX
 PR 11-MAR-2000; 2000EP-00105190.

XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX
 PI Schlingensiepen K, Schlingensiepen R;

XX
 DR WPI; 2001-604124/69.

XX
 PT Mixture useful in preparation of medicament for treating tumors and
 PT immune disorders, comprises an inhibitor or suppressor of expression of a
 PT gene, and a molecule binding to expression product of the gene.

XX
 PS Claim 16; Page 2; 16pp; English.

XX
 CC The invention relates to a mixture comprising an inhibitor or suppressor
 CC of a gene and a molecule binding to an expression product of that gene.
 CC The gene is selected from the group consisting of TGF-beta, erbB-2, MIA,
 CC c-jun, junB, c-fos, VCAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF-
 CC -kB 2. Molecules including drugs are used to modulate biological
 CC functions through gene products and their derivatives - like e.g.
 CC glycosylated, phosphorylated or otherwise modified gene products, have
 CC either stimulated or inhibited gene products and/or their derivatives.
 CC The mixture is useful in the preparation of a medicament for treating
 CC tumours, immune disorders or for improving organ or cell transplantation
 CC or cell expansion, where inhibition of tumour growth, improvement of
 CC organ or cell transplantation or cell expansion and enhancement or
 CC inhibition of immune response is enhanced in a supra-additive manner. The
 CC mixture is useful in drug target validation, i.e., to identify genes that
 CC are relevant for certain pathological state by testing the effect of the
 CC mixture on a cell system or organism. The present sequence is a human

CC oligonucleotide useful in drug target validation
XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 4
AEB01186
ID AEB01186 standard; DNA; 18 BP.
XX
AC AEB01186;
XX
DT 08-SEP-2005 (first entry)
XX
DE TGF-beta 2 inhibition oligonucleotide SEQ ID NO 30.
XX
KW pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
KW Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
KW TGF-beta antagonist; Vaccine.
XX
OS Synthetic.
XX
XX WO2005059133-A2.
XX
PD 30-JUN-2005.
XX
XX 20-DEC-2004; 2004WO-EP053604.
XX
PR 19-DEC-2003; 2003EP-00029367.
PR 05-FEB-2004; 2004US-0541771P.
XX
XX (ANTI-) ANTISENSE PHARMA GMBH.
XX
PI Schlingensiepen K, Schlingensiepen R;
XX
XX WPI; 2005-479334/48.
XX
XX Pharmaceutical composition useful for treating neoplasm, comprises
PT stimulators stimulating function of immune system and/or immune cells and
PT substances inhibiting cell proliferation and/or inducing cell death.
XX
PS Claim 4; SEQ ID NO 30; 46pp; English.

CC The invention relates to a pharmaceutical composition (PC) comprising one
CC or more stimulators that stimulate the function of immune system and/or
CC immune cells and one or more substances inhibiting cell proliferation
CC and/or inducing cell death. A pharmaceutical composition is useful for
CC treating neoplasms chosen from solid tumors; blood born tumors such as
CC leukemia, acute or chronic myeloid or lymphoblastic leukemia; tumor
CC metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder
CC carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma,
CC carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal
CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical
CC carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma,
CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver
CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell
CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma, small
CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, small
CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin
CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell
CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine
CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence
CC represents a TGF-beta 2 inhibition oligonucleotide.

XX
SQ Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTGTGA 18
Db 1 CGGCATGCTCTATTGTGA 18

RESULT 5
AAZ65511
ID AAZ65511 standard; DNA; 22 BP.
XX
AC AAZ65511;
XX
DT 30-MAR-2000 (first entry)
XX
DE Immunosuppressant inhibitor oligonucleotide TGF-beta-12-9/22-2263.
XX
KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
KW glomerulonephritis; acute respiratory distress syndrome; ss;
KW atherosclerosis.
XX
OS Unidentified.
XX
XX WO963975-A2.
XX
PD 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-EP004013.
XX
XX 10-JUN-1998; 98EP-00110709.
PR 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen K, Schlingensiepen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
XX
PS Claim 10; Fig 1; 30pp; English.

CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque

XX
SQ Sequence 22 BP; 4 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | |
Db 5 CGGCATGCTCTATTGTGA 22

RESULT 6

AAF82681
ID AAF82681 standard; DNA, 27 BP.
XX
AC AAF82681;
XX
DT 18-JUN-2001 (first entry)
XX
DE Human TGF-beta2 PCR primer #2.
XX
XX Human; androgen response element; ARE; cytostatic; gene therapy;
KW prostate-specific chimera enhancer; transcriptional regulation;
KW targeted gene expression; prostate cancer; prostate disorder;
KW prostate-specific antigen; PSA; transforming growth factor beta2;
KW TGF-beta2; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200127256-A2.
XX
XX 19-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028444.
XX
XX 14-OCT-1999; 99US-0159691P.
XX
XX 15-OCT-1999; 99US-0159730P.
XX
XX (REGC) UNIV CALIFORNIA SYSTEM.
XX
XX Wu L, Carey MF, Belldgrun AS;
XX
XX WPI; 2001-273768/28.
XX

XX New polynucleotide, useful for treating prostatic cancer, comprises
PT prostate specific chimera enhancer and proximal promoter sequence
PT operably linked to nucleic acid encoding heterologous polypeptide.
XX
XX Example 5; Page 73; 131pp; English.
XX
XX The present sequence was used in reverse transcriptase polymerase chain
CC reaction (RT-PCR) analysis of human prostate cancer cells. The invention
CC relates to an isolated polynucleotide comprising a prostate-specific
CC chimera enhancer (PSE) sequence and a proximal promoter sequence
CC operably linked to a nucleic acid segment that encodes a heterologous
CC polypeptide. The PSE contains an ARE and specifically activates
CC transcription of the nucleic acid segment in a mammalian prostate cell.
CC The construct is useful for the treatment of a prostate disorder or a
CC metastasized prostate cancer, such as hyperplasia or hyperproliferation
CC of prostate cells. It is also useful for directing the tissue-specific
CC expression of a heterologous polypeptide in a human prostate cell. The
CC construct may be administered by injection, infection, transformation,
CC liposome-mediated transfection, polybrene-mediated transfection, receptor
CC -mediated uptake or Ca-PO4-mediated transformation
XX
XX Sequence 27 BP; 5 A; 7 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTGA 18
| | | | | | | | | | | | | | | | | |
Db 3 CGGCATGCTCTATTGTGA 20

RESULT 7

AAV48940 standard; DNA, 20 BP.

AAZ65472
ID AAZ65472 standard; DNA, 16 BP.
XX
AC AAZ65472;
XX
DT 30-MAR-2000 (first entry)
XX
XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-9/1.

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
KW glomerulonephritis; acute respiratory distress syndrome; ss;
KW atherosclerosis.

XX Unidentified.

XX WO9963975-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-EF004013.
XX
XX 10-JUN-1998; 98EP-00110709.
XX
XX 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX

XX Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
XX
XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10, IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia, (non-)Hodgkin's lymphoma, carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX

XX Sequence 16 BP; 2 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCATGCTCTATTGTG 16
| | | | | | | | | | | | | | | |
Db 1 CGGCATGCTCTATTGTG 16

RESULT 8

AAV48940
ID AAV48940 standard; DNA, 20 BP.

XX AAV48940;
 AC
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-11.
 XX
 DE Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
 XX modulate; gene expression; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX EP856579-A1.
 PN
 XX
 XX 05-AUG-1998.
 PD
 XX
 XX 31-JAN-1997; 97EP-00101531.
 XX
 XX 31-JAN-1997; 97EP-00101531.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Brysch W;
 XX
 XX WPI; 1998-400910/35.
 DR
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 PT
 XX Claim 10; Fig 8a; 286pp; English.
 PS
 XX AAV48930-49007 represent antisense oligonucleotides directed against
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had
 CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine; do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, ErbB-2, junB, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 88.9%; Score 16; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GCATGCTATTGTA 18
 Db 1 GCATGCTATTGTA 16
 RESULT 9
 AAZ65448
 ID AAZ65448 standard; DNA; 20 BP.
 XX
 AC AAZ65448;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-8.
 XX
 DE Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 XX Unidentified.
 OS
 XX WO9963975-A2.
 PN
 XX 16-DEC-1999.
 PD
 XX 10-JUN-1999; 99WO-EP004013.
 XX
 XX 10-JUN-1999; 98EP-00110709.
 PR
 XX 25-JUL-1999; 98EP-00113974.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX
 XX WPI; 2000-097470/08.
 DR
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 PT
 XX Claim 5; Fig 1; 30pp; English.
 PS
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGF-beta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 88.9%; Score 16; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GCATGCTATTGTA 18
 Db 1 GCATGCTATTGTA 16
 RESULT 10
 AAZ65509
 ID AAZ65509 standard; DNA; 20 BP.
 XX
 AC AAZ65509;
 XX
 DT 30-MAR-2000 (first entry)
 XX

DE Immunosuppressant inhibitor oligonucleotide TGF-beta-12-9/20-2261.
XX
XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
KW glomerulonephritis; acute respiratory distress syndrome; ss;
KW atherosclerosis.
XX
XX Unidentified.
XX
XX
XX WO9963975-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-EP004013.
XX
XX 10-JUN-1998; 98EP-00110709.
XX 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
XX
XX Claim 10; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 88.9%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCATGCTCTATTG 16
Db 5 CGGCATGCTCTATTG 20
RESULT 11
ADI80184/c
ID ADI80184 standard; DNA; 20 BP.
XX
XX ADI80184;
XX
XX 22-APR-2004 (first entry)
DT
XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 185.
XX

KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
XX US2004006030-A1.
XX
XX 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX 02-JUL-2002; 2002US-00189267.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 185; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 88.9%; Score 16; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCATGCTCTATTG 16
Db 16 CGGCATGCTCTATTG 1
RESULT 12
ADI80039
ID ADI80039 standard; DNA; 20 BP.
XX
XX ADI80039;
XX
XX 22-APR-2004 (first entry)
DT
XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 40.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX

immune; ss; human.
Homo sapiens.
US2004006030-A1.
08-JAN-2004.
02-JUL-2002; 2002US-00189267.
02-JUL-2002; 2002US-00189267.
(ISIS-) ISIS PHARM INC.
Monia BP, Freier SM, Dobie KW;
WPI; 2004-081742/08.
New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.
Example 15; SEQ ID NO 40; 135pp; English.
The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.
Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 88.9%; Score 16; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGATGCTATTGTTG 16
Db 5 CGGATGCTATTGTTG 20
RESULT 13
AEB01185
ID AEB01185 standard; DNA; 20 BP.
AC AEB01185;
XX
XX
XX 08-SEP-2005 (first entry)
DE TGF-beta 2 inhibition oligonucleotide SEQ ID NO 29.
XX pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
KW Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
KW TGF-beta antagonist; Vaccine.
XX Synthetic.
XX

PN WO2005059133-A2.
XX 30-JUN-2005.
PD
XX
XX 20-DEC-2004; 2004WO-EP053604.
XX
XX 19-DEC-2003; 2003EP-00029367.
PR 03-FEB-2004; 2004US-0341771P.
XX
XX (ANTI-) ANTISENSE PHARMA GMBH.
XX
XX Schlingensiepen K, Schlingensiepen R;
PI WPI; 2005-479334/48.
XX
XX Pharmaceutical composition useful for treating neoplasm, comprises stimulators stimulating function of immune system and/or immune cells and substances inhibiting cell proliferation and/or inducing cell death.
PS Claim 4; SEQ ID NO 29; 46pp; English.
XX
XX The invention relates to a pharmaceutical composition (PC) comprising one or more stimulators that stimulate the function of immune system and/or immune cells and one or more substances inhibiting cell proliferation and/or inducing cell death. A pharmaceutical composition is useful for treating neoplasms chosen from solid tumors; blood born tumors such as leukemias, acute or chronic myeloid or lymphoblastic leukemia; tumor metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma, carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal carcinoma, epithelial carcinoma, esophageal carcinoma, cervical carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma, gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma, small papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, skin intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence represents a TGF-beta 2 inhibition oligonucleotide.
XX Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
SQ Query Match 88.9%; Score 16; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 GCATGCTATTGTTGTA 18
Db 1 GCATGCTATTGTTGTA 16
RESULT 14
ADI80242/c
ID ADI80242 standard; DNA; 20 BP.
XX
XX ADI80242;
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 243.
DE
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
PN
XX 08-JAN-2004.
PD

```
XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM, Dobie KW;
PI
XX
XX WPI; 2004-081742/08.
DR
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT
XX neurodegenerative disorder, or a disease involving hyperactivation of
PT
XX immune response.
XX
XX Example 16; SEQ ID NO 243; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC
XX in length targeted to, and which specifically hybridizes with, a nucleic
CC
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC
XX inhibits the expression of TGF-beta 2. The invention further relates to:
CC
XX a compound 8-80 nucleobases in length that specifically hybridizes with
CC
XX at least an 8-nucleobase portion of an active site on a nucleic acid
CC
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
CC
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC
XX tissues by contacting the cells or tissues with the compound so that
CC
XX expression of TGF-beta 2 is inhibited; treating an animal having a
CC
XX disease or condition associated with TGF-beta 2 by administering to the
CC
XX animal a therapeutic or prophylactic amount of the compound so that
CC
XX expression of TGF-beta 2 is inhibited; and screening an antisense
CC
XX compound. The antisense compound has cytostatic, neurotropic,
CC
XX neuroprotective, and immunosuppressive activities. The compound,
CC
XX composition and methods are useful for treating a disease or condition
CC
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC
XX cancer, a neurodegenerative disorder, or a disease or condition involving
CC
XX hyperactivation of an immune response. This polynucleotide sequence
CC
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 82.2%; Score 14.8; DB 12; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 1.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 CGGCATGCTATTGTGA 18
XX | | | | | | | | | |
XX Db 20 CGGCATGCTGATTTTATA 3
XX
XX RESULT 15
XX ADI80115
XX ID ADI80115 standard; DNA; 20 BP.
XX
XX AC ADI80115;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 116.
XX
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX
XX OS Mus musculus.
XX
XX PN US2004006030-A1.
XX
XX PD 08-JAN-2004.
XX
XX PF 02-JUL-2002; 2002US-00189267.
XX
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PR 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX
XX immune response.
XX
XX Example 16; SEQ ID NO 116; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX
XX tissues by contacting the cells or tissues with the compound so that
XX
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX
XX disease or condition associated with TGF-beta 2 by administering to the
XX
XX animal a therapeutic or prophylactic amount of the compound so that
XX
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX
XX compound. The antisense compound has cytostatic, neurotropic,
XX
XX neuroprotective, and immunosuppressive activities. The compound,
XX
XX composition and methods are useful for treating a disease or condition
XX
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX
XX hyperactivation of an immune response. This polynucleotide sequence
XX
XX represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 82.2%; Score 14.8; DB 12; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 1.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 CGGCATGCTATTGTGA 18
XX | | | | | | | | | |
XX Db 1 CGGCATGCTGATTTTATA 18
XX
XX Search completed: March 4, 2006, 02:31:45
XX Job time : 353.053 secs
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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:42:16 ; Search time 957.368 Seconds
(without alignments)
1187.494 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20
Sequence: 1 gctttcaccataattggaagc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1934910

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEnbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sv.*
12: gb_un.*
13: gb_vl.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6 A88384	A88384 Sequence 53
2	20	100.0	20	6 A90351	A90351 Sequence 53
3	20	100.0	20	6 BD065897	BD065897 An antisense
4	20	100.0	20	6 BD234910	BD234910 A method
5	20	100.0	20	6 CS123684	CS123684 Sequence
6	20	100.0	20	6 AX008981	AX008981 Sequence
7	20	100.0	20	6 AX252495	AX252495 Sequence
8	18	90.0	18	6 A89125	A89125 Sequence 12
9	18	90.0	18	6 BD066638	BD066638 An antisense
10	18	90.0	18	6 BD234924	BD234924 A method
11	18	90.0	18	6 AX008995	AX008995 Sequence
12	16	80.0	16	6 A89127	A89127 Sequence 12
13	16	80.0	16	6 BD066640	BD066640 An antisense
14	16	80.0	16	6 BD234926	BD234926 A method
15	16	80.0	16	6 AX008997	AX008997 Sequence
16	16	80.0	18	6 A40542	A40542 Sequence 79
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18	16	80.0	18	6 BD066580	BD066580 An antisense

19	16	80.0	18	6 BD234909	BD234909 A method
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21	16	80.0	18	6 AR232822	AR232822 Sequence
22	16	80.0	18	6 AX008980	AX008980 Sequence
23	16	80.0	18	6 AX030117	AX030117 Sequence
24	16	80.0	18	6 AX116438	AX116438 Sequence
25	15	75.0	15	6 A89126	A89126 Sequence 12
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39	13.2	66.0	20	6 AX785543	AX785543 Sequence
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41	13.2	66.0	24	6 AR149633	AR149633 Sequence
42	13.2	66.0	24	6 AR404763	AR404763 Sequence
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ALIGNMENTS

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LOCUS	A88384					
DEFINITION	A88384					
ACCESSION	A88384					
VERSION	A88384.1	GI:6736954				
KEYWORDS						
SOURCE	unidentified					
ORGANISM	unclassified sequences.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Brysch, W. and Schlingensiepen, K.					
TITLE	AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD					
JOURNAL	Patent: WO 9833904-A 532 06-AUG-1998;					
FEATURES	BIOSOURCE: GENE (DE); BRYSCH WOLFGANG (DE)					
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LOCUS	A90351					
DEFINITION	A90351					
ACCESSION	A90351					
VERSION	A90351.1	GI:6738865				
KEYWORDS						
SOURCE	unidentified					
ORGANISM	unclassified sequences.					

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REFERENCE 1 (bases 1 to 20)
AUTHORS Brysch,W.D. and Schlingensiepen,K.H.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 532 03-AUG-1998;
BIOGNOSTIK GES (DE)
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RESULT 3
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LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065897
VERSION BD065897.1 GI:22611500
KEYWORDS JP 2001511000-A/532.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 532 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/532
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 41;
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DB 1 GCTTTCACCAAAATTGGAAGC 20
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LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234910
VERSION BD234910.1 GI:130404680
KEYWORDS JP 2002517434-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 14 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/14
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PI KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
METHOD for stimulating the immune system
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DEFINITION Sequence 35 from Patent WO2005059133.
ACCESSION CS123684
VERSION CS123684.1 GI:70912177
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Schlingensiepen,K.H.
TITLE Combination therapy associating a tgf-beta antagonist with a
chemotherapeutic agent
JOURNAL Patent: WO 2005059133-A 35 30-JUN-2005;
Antisense Pharma GmbH (DE)
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Location/Qualifiers
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LOCUS AX008981 20 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 14 from Patent WO9963975.
ACCESSION AX008981
VERSION AX008981.1 GI:9996355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R.
AUTHORS A method for stimulating the immune system
TITLE Patent: WO 9963975-A 14 16-DEC-1999;
JOURNAL BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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LOCUS AX252495 20 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 5 from Patent WO0168146.
ACCESSION AX252495
VERSION AX252495.1 GI:15985766
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 Schlingensiepen, K.H. and Schlingensiepen, R.
AUTHORS Mixture comprising an inhibitor or suppressor of a gene and a
TITLE molecule binding to an expression product of that gene
JOURNAL Patent: WO 0168146-A 5 20-SEP-2001;
Biognostik Gesellschaft fuer biomolekulare Diagnostik mbH (DE)
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ACCESSION A89125
VERSION A89125.1 GI:6737695
KEYWORDS

SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1273 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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LOCUS BD066638 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066638
VERSION BD066638.1 GI:22612241
KEYWORDS JP 2001511000-A/1273.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1273 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1273
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PC C12N15/11, C07H21/04, A61K31/70
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DB 1 CTTTCACCAAAATTGGAAG 18
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LOCUS BD234924 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234924
VERSION BD234924.1 GI:33044694
KEYWORDS JP 2002517434-A/28.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 28 JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/28
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
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DEFINITION Sequence 28 from Patent WO9963975.
ACCESSION AX008995
VERSION AX008995.1 GI:9996369
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 28 DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)

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DEFINITION Sequence 1275 from Patent WO9833904.
ACCESSION A89127
VERSION A89127.1 GI:6737697
KEYWORDS
SOURCE
ORGANISM
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unclassified sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1275 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066640
VERSION BD066640.1 GI:22612243
KEYWORDS JP 2001511000-A/1275.
SOURCE
ORGANISM
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unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1275 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT
OS Unknown
PN JP 2001511000-A/1275
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
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Db 1 TCACCAAAATGGGAAGC 16

RESULT 14

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DEFINITION A method for stimulating the immune system.
ACCESSION BD234926
VERSION BD234926.1 GI:33044696
KEYWORDS JP 2002517434-A/30.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 16)

Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.

A method for stimulating the immune system

Patent: JP 2002517434-A 30 18-JUN-2002;

BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH

OS Homo sapiens (human)

PN JP 2002517434-A/30

PD 18-JUN-2002

PF 10-JUN-1999 JP 2000553044

PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI

KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI

BRYSCH

PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/

PC 00,A61P35/00;

PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A

method for stimulating the immune system

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DEFINITION Sequence 30 from Patent WO9963975.
ACCESSION AX008997
VERSION AX008997.1 GI:9996371
KEYWORDS
SOURCE Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 16)

Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.

A method for stimulating the immune system

Patent: WO 9963975-A 30 16-DEC-1999;

BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL

HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)

Location/Qualifiers

1..16

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DB 1 TCACCAAAATTGGAAGC 16

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Job time : 960.368 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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6	18	90.0	20	12	ADI80035
7	18	90.0	20	12	ADI80181
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9	16	80.0	18	2	AAQ78430
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17	14.2	71.0	32	2	AAV72954
18	14.2	71.0	40	12	ADP71056
19	13.8	69.0	17	4	AAH95671

C	20	13.8	69.0	19	10	ADP92715
C	21	13.8	69.0	19	10	ADP92603
C	22	13.8	69.0	29	3	AAA04270
C	23	13.8	69.0	37	9	ACF57163
C	24	13.8	69.0	40	13	ADU50752
C	25	13.8	69.0	40	13	ADU50751
C	26	13.6	68.0	33	6	ABX14388
C	27	13.2	66.0	20	4	ADL14558
C	28	13.2	66.0	20	10	ADD42186
C	29	13.2	66.0	20	10	ADD42188
C	30	13.2	66.0	20	10	ADD42190
C	31	13.2	66.0	20	10	ADD93796
C	32	13.2	66.0	20	12	ADK77402
C	33	13.2	66.0	20	12	ADK74986
C	34	13.2	66.0	20	14	AEA13360
C	35	13.2	66.0	21	9	ACH03553
C	36	13.2	66.0	22	8	ACC62420
C	37	13.2	66.0	23	10	ACF36660
C	38	13.2	66.0	23	12	ADJ93569
C	39	13.2	66.0	24	2	AAQ45017
C	40	13.2	66.0	24	2	AAV42144
C	41	13.2	66.0	24	2	AAV67008
C	42	13.2	66.0	24	6	ABQ09564
C	43	13.2	66.0	24	6	ABQ02831
C	44	13.2	66.0	24	6	ABQ09605
C	45	13.2	66.0	24	13	ADW08263

ALIGNMENTS

RESULT 1

AAV48943

ID AAV48943 standard; DNA; 20 BP.

XX AC AAV48943;

XX DT 15-OCT-1998 (first entry)

XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-14.

XX KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;

XX KW modulate; gene expression; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN EP856579-A1.

XX PD 05-AUG-1998.

XX PF 31-JAN-1997; 97EP-00101531.

XX PR 31-JAN-1997; 97EP-00101531.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen K, Brysch W;

XX DR WPI, 1998-400910/35.

XX PT Preparation of antisense oligonucleotide(s) which lack long runs of

XX PT consecutive guanosine or inosine - and have specific ratio of residues

XX PT able to form two or three hydrogen bonds, have greater activity and

XX PT reduced toxicity, used therapeutically or to modulate growth of cells in

XX PT culture.

XX PS Claim 10; Fig 8a; 286pp; English.

XX CC AAV48930-49007 represent antisense oligonucleotides directed against

XX CC transforming growth factor-beta2 (TGF-beta2). Of these, only

XX CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-

XX CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had

CC little effect. The oligonucleotides exemplify the invention. The
 CC specification describes oligonucleotides that contain 8-30 nucleotides,
 CC which contain at most 8 nucleotides that can each form three hydrogen
 CC bonds to cytosine, do not contain four consecutive nucleotides able to
 CC form three H-bonds each to four consecutive cytosines; do not contain two
 CC sequences of three consecutive nucleotides each able to form three H-
 CC bonds to three consecutive cytosines, and the ratio between residues able
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of
 CC genes, particularly the genes for p53, ErbB-2, JunB, JunD, TGF-beta 1 or
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
 CC keratinocytes). The oligonucleotides can also be used to analyse function
 CC of proteins (by altering their expression or activity) and
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for
 CC stimulating the immune system

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGGAAGC 20
 |||||
 DB 1 GCTTTCACCAAAATTGGAAGC 20

RESULT 2

AAZ65454
 ID AAZ65454 standard; DNA; 20 BP.

AC AAZ65454;

XX 30-MAR-2000 (first entry)

XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-14.

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumor; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX Unidentified.

XX WO963975-A2.

XX 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP004013.

XX 10-JUN-1998; 98EP-00110709.

XX 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

XX WPI; 2000-097470/08.

XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)

CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGF-beta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGGAAGC 20
 |||||
 DB 1 GCTTTCACCAAAATTGGAAGC 20

RESULT 3

AAID18719

ID AAD18719 standard; DNA; 20 BP.

XX AAD18719;

XX 18-DEC-2001 (first entry)

XX Human oligonucleotide #5, useful in drug target validation.

XX Human; TGF-beta; erbB-2; MIA; c-jun; junB; c-fos; VCAM; NF-kappaB p65;
 KW NF-kappaB p50; ICAM; VEGF; NF-kB 2; therapy; tumor; immune disorder;
 KW organ transplantation; cell expansion; drug target validation;
 KW antitumor; immunosuppressive; ss.

XX Homo sapiens.

XX EP1133988-A1.

XX 19-SEP-2001.

XX 11-MAR-2000; 2000EP-00105190.

XX 11-MAR-2000; 2000EP-00105190.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R;

XX WPI; 2001-604124/69.

XX Mixture useful in preparation of medicament for treating tumors and
 PT immune disorders, comprises an inhibitor or suppressor of expression of a
 PT gene, and a molecule binding to expression product of the gene.

XX Claim 16; Page 3; 16pp; English.

XX The invention relates to a mixture comprising an inhibitor or suppressor
 CC of a gene and a molecule binding to an expression product of that gene.
 CC The gene is selected from the group consisting of TGF-beta, erbB-2, MIA,
 CC c-jun, junB, c-fos, VCAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF-
 CC -kB 2. Molecules including drugs are used to modulate biological
 CC functions through gene products and their derivatives - like e.g.
 CC glycosylated, phosphorylated or otherwise modified gene products, have
 CC either stimulated or inhibited gene products and/or their derivatives.
 CC The mixture is useful in the preparation of a medicament for treating
 CC tumours, immune disorders or for improving organ or cell transplantation

CC or cell expansion, where inhibition of tumour growth, improvement of
 CC organ or cell transplantation or cell expansion and enhancement or
 CC inhibition of immune response is enhanced in a supra-additive manner. The
 CC mixture is useful in drug target validation, i.e., to identify genes that
 CC are relevant for certain pathological state by testing the effect of the
 CC mixture on a cell system or organism. The present sequence is a human
 CC oligonucleotide useful in drug target validation
 XX
 SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTTCCACCAATTGGAAGC 20
 |||||
 DB 1 GCTTTCCACCAATTGGAAGC 20

RESULT 4

AEBO1191
 ID AEB01191 standard; DNA; 20 BP.

AC AEB01191;

XX 08-SEP-2005 (first entry)

DT TGF-beta 2 inhibition oligonucleotide SEQ ID NO 35.

DE pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
 KW Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
 KW TGF-beta antagonist; Vaccine.

XX Synthetic.

XX WO2005059133-A2.

PN 30-JUN-2005.

XX 20-DEC-2004; 2004WO-EP053604.

PF 19-DEC-2003; 2003EP-00029367.

PR 05-FEB-2004; 2004US-0541771P.

XX (ANTI-) ANTISENSE PHARMA GMBH.

PA Schlingensiepen K, Schlingensiepen R;

XX WPI; 2005-479334/48.

DR Pharmaceuical composition useful for treating neoplasm, comprises
 XX stimulators stimulating function of immune system and/or immune cells and
 XX substances inhibiting cell proliferation and/or inducing cell death.

XX Claim 4; SEQ ID NO 35; 46pp; English.

XX The invention relates to a pharmaceutical composition (PC) comprising one
 CC or more stimulators that stimulate the function of immune system and/or
 CC immune cells and one or more substances inhibiting cell proliferation
 CC and/or inducing cell death. A pharmaceutical composition is useful for
 CC treating neoplasms chosen from solid tumors; blood born tumors such as
 CC leukemias, acute or chronic myeloid or lymphoblastic leukemia; tumor
 CC metastasis; benign tumors; or is chosen from bile duct carcinoma; bladder
 CC carcinoma; brain tumor; breast carcinoma; bronchogenic carcinoma;
 CC carcinoma of kidney; choriocarcinoma; cystadenocarcinoma; embryonal
 CC carcinoma; epithelial carcinoma; esophageal carcinoma; cervical
 CC carcinoma; colon carcinoma; colorectal carcinoma; endometrial carcinoma,
 CC gallbladder carcinoma; gastric carcinoma; head and neck carcinoma; liver
 CC carcinoma; lung carcinoma; medullary carcinoma; non-small cell
 CC bronchogenic/lung carcinoma; ovarian carcinoma; pancreas carcinoma;
 CC papillary carcinoma; papillary adenocarcinoma; prostate carcinoma, small
 CC intestine carcinoma; rectal carcinoma; renal cell carcinoma, skin
 CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell

CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine
 CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence
 CC represents a TGF-beta 2 inhibition oligonucleotide.

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTTCCACCAATTGGAAGC 20
 |||||
 DB 1 GCTTTCCACCAATTGGAAGC 20

RESULT 5

AAZ65468

ID AAZ65468 standard; DNA; 18 BP.

XX AAZ65468;

AC 30-MAR-2000 (first entry)

DT Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/1.

DE Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX Unidentified.

XX WO9963975-A2.

PN 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP004013.

PF 10-JUN-1998; 98EP-00110709.

PR 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

PA Schlingensiepen K, Schlingensiepen R, Brysch W;

XX WPI; 2000-097470/08.

DR Composition containing immune stimulant and inhibitor of agent that
 XX adversely affects the immune response, for treating cancers and
 XX infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress

CC syndrome and the formation of atherosclerotic plaque
XX Sequence 18 BP; 6 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
SQ Query Match 90.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGAAG 19
DB 1 CTTTCACCAAAATTGGAAG 18

RESULT 6
ADI80035
ID ADI80035 standard; DNA; 20 BP.
XX AC ADI80035;
XX DT 22-APR-2004 (first entry)
XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 36.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; human.
XX OS Homo sapiens.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 15; SEQ ID NO 36; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC molecule encoding TGF-beta 2; a composition comprising the compound and
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGGA 18
DB 3 GCTTTCACCAAAATTGGA 20

RESULT 7
ADI80181/c
ID ADI80181 standard; DNA; 20 BP.
XX AC ADI80181;
XX XX DT 22-APR-2004 (first entry)
XX DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 182.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; human.
XX OS Homo sapiens.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 182; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC molecule encoding TGF-beta 2; a composition comprising the compound and
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTACCAAAATTGGAA 18
 DB 18 GCTTTACCAAAATTGGAA 1

RESULT 8
 AAZ65470
 ID AAZ65470 standard; DNA; 16 BP.
 XX AC AAZ65470;
 XX DT 30-MAR-2000 (first entry)
 XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/3.
 XX KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX OS Unidentified.
 XX PN WO9963975-A2.
 XX PD 16-DEC-1999.
 XX PF 10-JUN-1999; 99WO-EP004013.
 XX PR 10-JUN-1998; 98EP-00110709.
 XX PR 25-JUL-1998; 98EP-00113974.
 XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX PI Schlingensiepen K, Schlingensiepen R, Brysch W;
 XX WPI; 2000-097470/08.
 XX PT Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 XX PS Claim 5; Fig 1; 30pp; English.
 XX CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX SQ Sequence 16 BP; 6 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCACCAAAATTGGAAGC 20
 DB 1 TCACCAAAATTGGAAGC 16

RESULT 9
 AAQ78430
 ID AAQ78430 standard; DNA; 18 BP.
 XX AC AAQ78430;
 XX DT 25-MAR-2003 (revised)
 XX DT 27-JUN-1995 (first entry)
 XX DE TGF-beta gene phosphorothioate antisense oligonucleotide.
 XX KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 KW immunosuppression; oligonucleotide; ss.
 XX OS Synthetic.
 XX PN WO9425588-A2.
 XX PD 10-NOV-1994.
 XX PF 29-APR-1994; 94WO-EP001362.
 XX PR 30-APR-1993; 93EP-00107089.
 XX PR 13-MAY-1993; 93EP-00107849.
 XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 XX PI Bogdahn U;
 XX DR WPI; 1994-358266/44.
 XX PT New transforming growth factor beta anti-sense oligonucleotide(s) - for
 PT treating immunosuppression, tumours, etc.
 XX PS Claim 6; Page 46; 74pp; English.
 XX CC The antisense oligonucleotides are useful in the treatment of tumours in
 CC which expression of TGF-beta is of relevance for pathogenicity and/or
 CC inhibition of pathological angiogenesis. They are used especially for the
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-078488. The sequences given in GENESQ files
 CC AAQ78352-078407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCACCAAAATTGGAAGC 20
 DB 1 TCACCAAAATTGGAAGC 16

RESULT 10
 AAZ65453
 ID AAZ65453 standard; DNA; 18 BP.
 XX

AC AA265453;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-13.
 XX
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 XX WO9963975-A2.
 PN
 XX
 XX 16-DEC-1999.
 PD
 XX
 XX 10-JUN-1999; 99WO-EP004013.
 PF
 XX
 XX 10-JUN-1998; 98EP-00110709.
 PR
 XX 25-JUL-1998; 98EP-00113974.
 PR
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI
 XX WPI; 2000-097470/08.
 DR
 XX
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 PT
 XX
 PS Claim 5; Fig 1; 30pp; English.
 XX
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TCACCAAAATTTGAAGC 20
 Db 1 TCACCAAAATTTGAAGC 16
 RESULT 11
 AEB01190
 ID AEB01190 standard; DNA; 18 BP.
 XX
 AC AEB01190;
 XX

DT 08-SEP-2005 (first entry)
 XX
 DE TGF-beta 2 inhibition oligonucleotide SEQ ID NO 34.
 XX
 KW pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
 KW immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
 KW TGF-beta antagonist; Vaccine.
 XX
 OS Synthetic.
 OS
 PN WO2005059133-A2.
 XX
 XX 30-JUN-2005.
 PD
 XX
 XX 20-DEC-2004; 2004WO-EP053604.
 PF
 XX
 XX 19-DEC-2003; 2003EP-00029367.
 PR
 XX 05-FEB-2004; 2004US-0541771P.
 PR
 XX (ANTI-) ANTISENSE PHARMA GMBH.
 PA
 XX Schlingensiepen K, Schlingensiepen R;
 PI
 XX WPI; 2005-479334/48.
 DR
 XX
 XX Pharmaceutical composition useful for treating neoplasm, comprises
 PT stimulants stimulating function of immune system and/or immune cells and
 PT substances inhibiting cell proliferation and/or inducing cell death.
 PT
 XX
 PS Claim 4; SEQ ID NO 34; 46pp; English.
 XX
 CC The invention relates to a pharmaceutical composition (PC) comprising one
 CC or more stimulants that stimulate the function of immune system and/or
 CC immune cells and one or more substances inhibiting cell proliferation
 CC and/or inducing cell death. A pharmaceutical composition is useful for
 CC treating neoplasms chosen from solid tumors; blood born tumors such as
 CC leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor
 CC metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder
 CC carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma,
 CC carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal
 CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical
 CC carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma,
 CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver
 CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell
 CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma,
 CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, small
 CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin
 CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell
 CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine
 CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence
 CC represents a TGF-beta 2 inhibition oligonucleotide.
 XX
 SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 80.0%; Score 16; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 TCACCAAAATTTGAAGC 20
 Db 1 TCACCAAAATTTGAAGC 16
 RESULT 12
 AA265469
 ID AA265469 standard; DNA; 15 BP.
 XX
 AC AA265469;
 XX
 XX 30-MAR-2000 (first entry)
 DT
 XX
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-14/2.
 XX

KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumor; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.

XX Unidentified.

XX WO9963975-A2.

XX 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP004013.

XX 10-JUN-1998; 98EP-00110709.

XX 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

XX WPI; 2000-097470/08.

XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
 CC used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGF-beta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as anti-
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque

XX Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CACCAAAATGGGAAGC 20

Db 1 CACCAAAATGGGAAGC 15

RESULT 13

AAD48552/c

ID AAD48552 standard; DNA; 20 BP.

XX AAD48552;

XX 24-FEB-2003 (first entry)

XX Chicken lysozyme gene fragment sequencing PCR primer, lys056for.

XX Lysozyme gene expression control region; chromosomal positional effect;
 KW transgene; avian cell; PCR; primer; chicken; ss.

XX OS Gallus sp.
 XX WO200279447-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-US009866.

XX 30-MAR-2001; 2001US-0280004P.

XX 03-AUG-2001; 2001US-00922549.

XX 25-JAN-2002; 2002US-0351550P.

XX (AVIG-) AVIGENICS INC.

XX Rapp JC;

XX WPI; 2003-046807/04.

XX New isolated or recombinant nucleic acid for reducing the chromosomal
 PT positional effect of a transgene, comprises an isolated avian lysozyme
 PT gene expression control region.

XX Example 1; Fig 1; 89pp; English.

XX The invention relates to an isolated or recombinant nucleic acid or DNA
 CC molecule comprising an isolated avian lysozyme gene expression control
 CC region operably linked to a nucleic acid insert encoding a polypeptide.
 CC The nucleic acid is useful for reducing the chromosomal positional effect
 CC of a transgene operably linked to the lysozyme gene expression control
 CC region and transfected into a recipient avian cell. The present sequence
 CC is a PCR primer used for sequencing chicken lysozyme gene expression
 CC control region

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 20;

Best Local Similarity 84.2%; Pred. NO. 3.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GCTTTTCCCAAAATGGGAAG 19

Db 20 GCTGTCCCAACATGGGAAG 2

RESULT 14

ADK78448/c

ID ADK78448 standard; DNA; 20 BP.

XX ADK78448;

XX 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5782.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
 KW diabetic neuropathy; arthritic pain; migraine headache;
 KW infantile epilepsy; ataxia; ss.

XX Synthetic.

XX WO2004016754-A2.

XX 26-FEB-2004.

XX 14-AUG-2003; 2003WO-US025465.

XX 14-AUG-2002; 2002US-0403416P.

XX (PHAA) PHARMACIA CORP.

XX Roberds SL;

XX

DR WPI; 2004-203785/19.
XX New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 5782; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 71.0%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCTTTCACCAAAATGGGAG 19
DB 19 GCTTCCAGCAATGGGAG 1
RESULT 15
ADK78529/c
ID ADK78529 standard; DNA; 20 BP.
XX
AC ADK78529;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5863.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberts SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 5863; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a

nucleic acid molecule encoding Nav1.3, where the antisense compound
specifically hybridizes with and inhibits the expression of Nav1.3. The
compound and composition are useful for treating a disease or condition
associated with Nav1.3, e.g. pain including but not limited to
neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
pain from burns, migraine headache, cluster headache, mild-to-moderate
headache; seizure disorder such as childhood seizure disorder, including
but not limited to neonatal or infantile epilepsy; or ataxia. The present
sequence represents a chimeric phosphorothioate oligonucleotide with
2'MOE wings and a deoxy gap. Used during the antisense inhibition of
human Nav1.3 expression, the oligonucleotides are designed to target
different regions of the human Nav1.3 RNA.
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 71.0%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCTTTCACCAAAATGGGAG 19
DB 20 GCTTCCAGCAATGGGAG 2
Search completed: March 4, 2006, 02:31:42
Job time : 393.947 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:46:27 ; Search time 3170.53 Seconds
(without alignments)
295.138 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gctttcaccattggaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 106998

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.4	67.0	34	1	AV852639
C 2	12.8	64.0	25	10	CG729682
C 3	12.8	64.0	31	1	AI034270
C 4	12.6	63.0	33	9	BZ769257
5	12.4	62.0	35	9	AZ336391
6	12.2	61.0	26	9	BH863411
7	12.2	61.0	34	9	AZ645914
C 8	12	60.0	21	9	AZ308115
C 9	12	60.0	27	10	AG204809
C 10	12	60.0	32	9	BH904979
C 11	12	60.0	32	10	AJ600156
C 12	11.8	59.0	31	1	AU255583
C 13	11.8	59.0	32	5	BQ587054
C 14	11.8	59.0	36	9	BZ661352
15	11.8	59.0	37	1	AI823627
16	11.8	59.0	40	1	AA887375
17	11.8	59.0	40	1	AA961031
18	11.6	58.0	31	11	CR395105
19	11.6	58.0	34	9	AZ789746
C 20	11.6	58.0	34	11	CR358544
C 21	11.6	58.0	35	9	BH854633
22	11.4	57.0	19	1	AI790036

C 23	11.4	57.0	31	9	BH792339
24	11.4	57.0	34	9	BH905278
25	11.4	57.0	36	10	CZ469111
26	11.2	56.0	28	11	TA285H02Q
C 27	11.2	56.0	29	9	CC794724
C 28	11.2	56.0	32	9	AZ309847
29	11.2	56.0	33	11	DR23D20T
30	11.2	56.0	34	6	CF302443
C 31	11.2	56.0	34	9	AZ761083
C 32	11.2	56.0	34	9	AZ781725
C 33	11.2	56.0	36	9	AZ864054
C 34	11.2	56.0	36	10	CL528503
C 35	11.2	56.0	37	9	BH811021
C 36	11.2	56.0	37	9	BH865074
C 37	11.2	56.0	37	9	BH903531
C 38	11.2	56.0	38	1	AU259281
C 39	11.2	56.0	39	9	BH856768
C 40	11	55.0	21	10	AJ596091
41	11	55.0	28	10	CZ469769
42	11	55.0	28	10	CZ471273
C 43	11	55.0	29	9	AZ580321
44	11	55.0	34	9	AZ658401
C 45	11	55.0	35	10	CZ471370

ALIGNMENTS

RESULT 1
AV852639/c 34 bp mRNA linear EST 08-NOV-2001
LOCUS AV852639 Nori Satoh unpublished cDNA library, larva Ciona
DEFINITION intestinalis cDNA clone rcilv19c08 3', mRNA sequence.
ACCESSION AV852639
VERSION AV852639.1 GI:16837973
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
REFERENCE 1 (bases 1 to 34)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
Location/Qualifiers
1..34
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcilv19c08"
/tissue type="whole animal"
/dev_stage="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"

ORIGIN

Query Match 67.0%; Score 13.4; DB 1; Length 34;
Best Local Similarity 93.3%; Pred. No. 8e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TTCACCAAAATGGAA 18
|||||
DB 32 TTCACCAAAATGGAA 18

RESULT 2
CG729682/c

JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g35820.
Class: TDNA tagged.

FEATURES
source

Location/Qualifiers
1..33
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK 141859.37.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 63.0%; Score 12.6; DB 9; Length 33;
Best Local Similarity 78.9%; Pred. No. 2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATGGAAG 19
||||| ||| ||| |||
DB 32 GCTTCCAGCAAGTTGTAG 14

RESULT 5

AZ336391 35 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
clone UUGC1M0066G07 R, genomic survey sequence.

ACCESSION AZ336391
VERSION AZ336391.1 GI:10405642
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0066 row: G column: 07

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 35.

FEATURES

source

Location/Qualifiers
1..35
/organism="Mus musculus"

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0066G07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 62.0%; Score 12.4; DB 9; Length 35;
Best Local Similarity 92.9%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATG 15
||||| ||| ||| |||
DB 1 CTATCACCAAAATG 14

RESULT 6

BH863411

LOCUS

DEFINITION

BH863411 26 bp DNA linear GSS 05-AUG-2002
SALK_093836 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093836, genomic survey sequence.

ACCESSION BH863411

VERSION BH863411.1 GI:22099002

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 26)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers
1..26
/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="SALK 093836"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 26;
 Best Local Similarity 82.4%; Pred. No. 3.1e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTCACCAAAATTGGAGC 20
 |||||
 Db 9 TACAGCAAAATTGGAGC 25

RESULT 7

AZ645914
 LOCUS 34 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM05111K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0511K08 R, genomic survey sequence.

ACCESSION AZ645914
 VERSION 1
 KEYWORDS GSS.
 SOURCE AZ645914.1 GI:11775868

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 34)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0511 row: K column: 08

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 34.

FEATURES

Source

1..34
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0511K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 34;
 Best Local Similarity 82.4%; Pred. No. 3.2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGAA 18
 |||||
 Db 2 CTTTCACCAAAATTGGAA 18

RESULT 8

AZ308115
 LOCUS 21 bp DNA linear GSS 29-SEP-2000
 DEFINITION IM0010J17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0010J17 R, genomic survey sequence.

ACCESSION AZ308115
 VERSION 1
 KEYWORDS GSS.
 SOURCE AZ308115.1 GI:10347784

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0010 row: J column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

Source

1..21
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0010J17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number-inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTTCACCAAT 13
|||||
DB 20 GTTTCACCAAT 9

RESULT 9

AG204809/c

LOCUS

DEFINITION Pan troglodytes DNA, clone: RP43-090L01.T7, genomic survey sequence.

ACCESSION

AG204809

VERSION

AG204809.1 GI:45236984

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

REFERENCE

1

AUTHORS

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE

BAC end sequences of Library RP-43

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 27)

AUTHORS

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE

Direct Submission

JOURNAL

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

REFERENCE

(E-mail: redstone@mail.krribb.re.kr URL: http://pbs.grc.krribb.re.kr/, Tel: 82-42-866-7181, Fax: 82-42-860-4409)

COMMENT

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

FEATURES

Location/Qualifiers

1..27

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-090L01.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match

Best Local Similarity 60.0%; Score 12; DB 10; Length 27;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTTTCCACCAATGGAAGC 20

DB 26 GCTTTCCACCAATGGAAGC 7
|||||

RESULT 10

BH904979/c

LOCUS

DEFINITION

Arabidopsis thaliana genomic clone SALK_105414.53.00.x, genomic survey sequence.

ACCESSION

BH904979

VERSION

BH904979.1 GI:23717726

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

REFERENCE

1 (bases 1 to 32)

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of

At4g01820.

FEATURES

Location/Qualifiers

1..32

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_105414.53.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

Best Local Similarity 60.0%; Score 12; DB 9; Length 32;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTTTCCACCAATGGAAGC 20

|||||

DB 31 GCTTTTACATATAGAAAC 12

RESULT 11

AJ600156

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence, right border, clone

501C03, genomic survey sequence.

ACCESSION

AJ600156

VERSION

AJ600156.1 GI:37949784

KEYWORDS

GSS; right border; T-DNA flanking sequence.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

REFERENCE

1

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of

At4g01820.

FEATURES

Location/Qualifiers

1..32

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_105414.53.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

Best Local Similarity 60.0%; Score 12; DB 9; Length 32;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTTTCCACCAATGGAAGC 20

|||||

DB 31 GCTTTTACATATAGAAAC 12

RESULT 12

AJ600156

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence, right border, clone

501C03, genomic survey sequence.

ACCESSION

AJ600156

VERSION

AJ600156.1 GI:37949784

KEYWORDS

GSS; right border; T-DNA flanking sequence.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

REFERENCE

1

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of

At4g01820.

FEATURES

Location/Qualifiers

1..32

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_105414.53.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

Best Local Similarity 60.0%; Score 12; DB 9; Length 32;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTTTCCACCAATGGAAGC 20

|||||

DB 31 GCTTTTACATATAGAAAC 12

```

REFERENCE
AUTHORS      Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
              Chauvin, S., Bechold, N., Cruaud, C., DeRose, R., Pelletier, G.,
              Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE        T-DNA integration into the Arabidopsis genome depends on sequences
              of pre-insertion sites
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED       12446565
LOCUS        2 (bases 1 to 32)
REFERENCE    Balzerque, S.
AUTHORS      Direct Submission
TITLE        Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
              Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).
FEATURES     Location/Qualifiers
              1..32
                  /organism="Arabidopsis thaliana"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:3702"
                  /clone="501C03"
                  /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                  /ecotype="Wassilewskija"
misc_feature 1..32
              /notes="T-DNA flanking sequence
              right border"
ORIGIN
Query Match      60.0%; Score 12; DB 10; Length 32;
Best Local Similarity 75.0%; Pred. NO. 4e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATGGAAG 20
    ||||| ||||| |||||
Db 1 GCTTTCCTCACTGGAGC 20

RESULT 12
AU255583/c
LOCUS          31 bp mRNA linear EST 25-APR-2002
DEFINITION    AU255583 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0005815 3', mRNA sequence.
ACCESSION     AU255583
VERSION       AU255583.1 GI:20318461
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     Kato, K. and Matoba, R.
AUTHORS      Generation of expressed sequence tags from mouse brain
              Unpublished (2002)
TITLE        Contact: Kikuya Kato
              Graduate School of Biological Sciences
              Nara Institute of Science and Technology
              8916-5 Takayama, Ikoma, Nara 630-0101, Japan
              Tel: 81-743-72-5581
              Fax: 81-743-72-5589
              Email: kkatob@bs.aist-nara.ac.jp,
              URL: http://love2.aist-nara.ac.jp/BED/index.html.
              Location/Qualifiers
FEATURES
source
1..31
    /organism="Mus musculus"
    /mol_type="mRNA"
    /db_xref="taxon:10090"
    /clone="BED0005815"
    /tissue_type="brain"
    /clone_lib="3'-directed mouse cDNA library"
ORIGIN
Query Match      59.0%; Score 11.8; DB 1; Length 31;
Best Local Similarity 86.7%; Pred. NO. 5e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTCACCAAAATGGA 17
    ||||| ||||| |||||
Db 17 TTGACTAAATGGA 3

RESULT 13
BO587054/c
LOCUS          32 bp mRNA linear EST 06-DEC-2002
DEFINITION    BO587054 024-011-H11-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-011-H11 5-PRIME, mRNA sequence.
ACCESSION     BO587054
VERSION       BO587054.1 GI:26116636
KEYWORDS      EST.
SOURCE        Beta vulgaris
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              Caryophyllales; Amaranthaceae; Beta.
REFERENCE     1 (bases 1 to 32)
AUTHORS      Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
              Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
              and Radelof, U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
              Plant J. 32 (5), 845-857 (2002)
JOURNAL       12472698
PUBMED       Contact: Weishaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaar@mpiz-koeln.mpg.de
              Insert Length: 32 Std Error: 0.00
              Plate: 11 row: H column: 11
              Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
              Location/Qualifiers
FEATURES     1..32
              /organism="Beta vulgaris"
              /mol_type="mRNA"
              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:185812"
              /db_xref="taxon:161934"
              /clone="024-011-H11"
              /tissue_type="leaf"
              /lab_host="EMDH108"
              /clone_lib="MP1Z-ADIS-024-leaf"
              /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
              cDNA library from sugar beet. Library provided by KWS
              Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              Project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
              Location/Qualifiers
FEATURES
Query Match      59.0%; Score 11.8; DB 5; Length 32;

```

Best Local Similarity 86.7%; Pred. No. 5.1e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 2 CTTTCACCAAAATGG 16

Db 23 CTTTCACCTATATGG 9

RESULT 14

BZ661352

LOCUS

DEFINITION

BZ661352 36 bp DNA linear GSS 31-JAN-2003
SALK_024821.36.20.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_024821.36.20.x, genomic
survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BZ661352.1 GI:28174499

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

JOURNAL

COMMENT

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g17360.
Class: TDNA tagged.

FEATURES

source

1..36

Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_024821.36.20.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

Best Local Similarity 86.7%; Pred. No. 5.1e+05;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTCACCAAAATGG 17

Db 1 TCTGACCAAAATGG 15

RESULT 15

A1823627

LOCUS

DEFINITION

A1823627 37 bp mRNA linear EST '21-DEC-1999
w185e02.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2400122 3,
similar to SW.6B13 HUMAN Q14344 GUANINE NUCLEOTIDE-BINDING PROTEIN,
ALPHA-13 SUBUNIT. ?; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

A1823627.1 GI:5444298

EST

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 37)

NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher Moshaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

cDNA Library Arrayed by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1024 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1..37

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2400122"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/clone_lib="NCI CGAP Kid12"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not 1; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid12 was

prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneIDs 1323912-1325831, 1471368-1472903 and

1492104-1493255). Subtraction by Bento Soares and M.

Fatima Bonaldo."

ORIGIN

Query Match

Best Local Similarity 59.0%; Score 11.8; DB 1; Length 37;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTCACCAAAATGG 18

Db 11 TTCACCAAAATGG 25

Search completed: March 4, 2006, 03:38:57

Job time : 3174.53 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:32 ; Search time 76.8421 Seconds
(without alignments)
462.653 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gcttcacaaattggaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1198766

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/68 COMB.seq.*
5: /cgn2_6/prodata/1/ina/H COMB.seq.*
6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	18	3	US-08-535-249-79
2	14.2	71.0	25	3	US-09-396-196G-6827
3	13.8	69.0	29	3	US-09-304-232-470
4	13.2	66.0	24	2	US-08-465-590-42
5	13.2	66.0	24	3	US-08-711-417C-42
6	13.2	66.0	24	3	US-09-723-909-42
7	13.2	66.0	24	6	PCF-US93-08743-42
8	13.2	66.0	25	3	US-09-396-196G-122784
9	12.8	64.0	19	3	US-09-696-791-4062
10	12.8	64.0	19	3	US-09-696-791-4063
11	12.8	64.0	25	3	US-09-396-196G-71637
12	12.8	64.0	25	3	US-09-396-196G-71638
13	12.8	64.0	25	3	US-09-396-196G-71639
14	12.8	64.0	25	3	US-09-396-196G-71640
15	12.8	64.0	25	3	US-09-396-196G-71641
16	12.8	64.0	25	3	US-09-396-196G-71642
17	12.8	64.0	26	2	US-08-118-387-4
18	12.8	64.0	29	2	US-08-306-871-39
19	12.8	64.0	29	2	US-08-569-959-39
20	12.8	64.0	30	3	US-08-544-381B-137
21	12.6	63.0	21	2	US-08-814-806-12
22	12.6	63.0	21	3	US-09-293-854-12
23	12.6	63.0	25	3	US-09-396-196G-16724
24	12.6	63.0	25	3	US-09-396-196G-18361

25	12.6	63.0	25	3	US-09-396-196G-40788	Sequence 40788, A
26	12.6	63.0	25	3	US-09-396-196G-62362	Sequence 62362, A
27	12.6	63.0	25	3	US-09-396-196G-81441	Sequence 81441, A
28	12.6	63.0	25	3	US-09-396-196G-81442	Sequence 81442, A
29	12.6	63.0	25	3	US-09-396-196G-81443	Sequence 81443, A
30	12.6	63.0	25	3	US-09-396-196G-81444	Sequence 81444, A
31	12.6	63.0	27	3	US-09-012-087A-40	Sequence 40, Appl
32	12.6	63.0	27	3	US-09-481-620A-58	Sequence 58, Appl
33	12.6	63.0	27	3	US-09-781-804-39	Sequence 39, Appl
34	12.6	63.0	28	3	US-09-589-483-6	Sequence 6, Appl
35	12.6	63.0	28	3	US-09-589-777C-6	Sequence 196, Appl
36	12.6	63.0	30	3	US-08-444-818-196	Sequence 2, Appl
37	12.6	63.0	38	3	US-09-231-077D-2	Sequence 31, Appl
38	12.4	62.0	20	3	US-09-629-645A-31	Sequence 9005, Ap
39	12.2	61.0	25	3	US-09-396-196G-9647	Sequence 9647, Ap
40	12.2	61.0	25	3	US-09-396-196G-13788	Sequence 13788, A
41	12.2	61.0	25	3	US-09-396-196G-13789	Sequence 13789, A
42	12.2	61.0	25	3	US-09-396-196G-18088	Sequence 18088, A
43	12.2	61.0	25	3	US-09-396-196G-18089	Sequence 18089, A
44	12.2	61.0	25	3	US-09-396-196G-127149	Sequence 127149, A
45	12.2	61.0	25	3	US-09-396-196G-127149	Sequence 127149, A

ALIGNMENTS

RESULT 1

US-08-535-249-79
; Sequence 79, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-79

Query Match 80.0%; Score 16; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCACCAAAATTGGAAGC 20
DB 1 TCACCAAAATTGGAAGC 16

RESULT 2
US-09-396-196G-6827
; Sequence 6827, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6827
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-6827

Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGAAGC 20
DB 5 CTTTCAGCAAGTTAGGAGC 23

RESULT 3
US-09-304-232-470/c
; Sequence 470, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; TITLE OF INVENTION: Hypertension
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 470
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GH2BX3 126
US-09-304-232-470

Query Match 69.0%; Score 13.8; DB 3; Length 29;
Best Local Similarity 78.9%; Pred. No. 9.2e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTTTCACCAAAATTGGAAG 19
DB 25 GTTTTCACCCGTTGGAAG 7

RESULT 4
US-08-465-590-42
; Sequence 42, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MPG-006C2DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-465-590-42

Query Match 66.0%; Score 13.2; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTTCACCAAAATTGGAAGC 20
DB 5 TTTAACCAATTGGAAGC 22

RESULT 5
US-08-711-417C-42
; Sequence 42, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-08-711-417C-42

Query Match 66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTCACCAATTGGGAAGC 20
||| ||||| |||||
DB 5 TTTAACCAATTGGGAAGC 22

RESULT 6
US-09-723-909-42
Sequence 42, Application US/097233909
Patent No. 6630141
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA: US/09/723,909
FILING DATE: 28-NOV-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417
FILING DATE: 05-Sep-1996
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-723-909-42

Query Match 66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTCACCAATTGGGAAGC 20
||| ||||| |||||
DB 5 TTTAACCAATTGGGAAGC 22

RESULT 7
PCT-US93-08743-42
Sequence 42, Application PC/TUS9308743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 946,233
FILING DATE: 14-SEP-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-08743-42

Query Match 66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTCACCAATTGGGAAGC 20
||| ||||| |||||
DB 5 TTTAACCAATTGGGAAGC 22

```
RESULT 8
US-09-396-196G-122784
; Sequence 122784, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-122784

Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTCCACCAAAATTGGAAGC 20
    ||||| |||||
Db 4 TTTCACTACAATGGAAGC 21

RESULT 9
US-09-696-791-4062/c
; Sequence 4062, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4062
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-4062

Query Match      64.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGA 17
    ||||| |||||
Db 19 CTTTAAACAATTTGGA 4

RESULT 10
US-09-696-791-4063/c
; Sequence 4063, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
```

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; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4063
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-4063

Query Match      64.0%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGA 17
    ||||| |||||
Db 18 CTTTAAACAATTTGGA 3

RESULT 11
US-09-396-196G-71637
; Sequence 71637, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71637

Query Match      64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTTTACCAAAATTGG 16
    ||||| |||||
Db 10 GCTGTACCAAAATTGG 25

RESULT 12
US-09-396-196G-71638
; Sequence 71638, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71638
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71639

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0;

QY 1 GCTTTCACCAAAATTGG 16
||| ||||| |||||
DB 8 GCTGTCAACCAATTGG 23

RESULT 13
US-09-396-196G-71639
; Sequence 71639, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71639
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71639

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0;

QY 1 GCTTTCACCAAAATTGG 16
||| ||||| |||||
DB 7 GCTGTCAACCAATTGG 22

RESULT 14
US-09-396-196G-71640
; Sequence 71640, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71640
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71640

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0;

QY 1 GCTTTCACCAAAATTGG 16

DB 4 GCTGTCAACCAATTGG 19
||| ||||| |||||

RESULT 15
US-09-396-196G-71641
; Sequence 71641, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71641

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0;

QY 1 GCTTTCACCAAAATTGG 16
||| ||||| |||||
DB 2 GCTGTCAACCAATTGG 17

Search completed: March 4, 2006, 02:07:26
Job time : 77.8421 secs

Thru Side Edge Blank (upside)
(photo)

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:58:42 ; Search time 495.789 Seconds
(without alignments)
88.444 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20

Sequence: 1 gcttcaccaaatggaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11581468

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.New.*

- 1: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq1.*
- 7: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq1.*
- 9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq2.*
- 11: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq3.*
- 12: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq4.*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	16.4	82.0	25	12	US-11-121-849-529681 Sequence 529681,
2	15.2	76.0	25	12	US-11-121-849-447577 Sequence 447577,
3	15.2	76.0	25	12	US-11-136-527-278180 Sequence 278180,
4	15	75.0	25	12	US-11-121-849-634116 Sequence 634116,
5	14.8	74.0	25	12	US-11-121-849-583444 Sequence 583444,
6	14.4	72.0	24	8	US-10-310-914A-323453 Sequence 323453,
7	14.4	72.0	25	12	US-11-121-849-206297 Sequence 206297,
8	14.4	72.0	25	12	US-11-121-849-206298 Sequence 206298,
9	14.4	72.0	25	12	US-11-121-849-206856 Sequence 206856,
10	14.4	72.0	25	12	US-11-121-849-206857 Sequence 206857,
11	14.2	71.0	25	8	US-10-310-914A-1191627 Sequence 1191627,
12	14.2	71.0	25	12	US-11-121-849-191 Sequence 191, App
13	14.2	71.0	25	12	US-11-121-849-345854 Sequence 345854,
14	14.2	71.0	25	12	US-11-121-849-673774 Sequence 673774,
15	14.2	71.0	25	12	US-11-121-849-673775 Sequence 673775,
16	14.2	71.0	25	12	US-11-121-849-673776 Sequence 673776,
17	14.2	71.0	25	12	US-11-121-849-673777 Sequence 673777,
18	13.8	69.0	19	10	US-11-101-244-1430638 Sequence 1430638,
19	13.8	69.0	19	11	US-11-083-784-1430638 Sequence 1430638,
20	13.8	69.0	20	8	US-10-310-914A-791928 Sequence 791928,

c 21	13.8	69.0	23	8	US-10-310-914A-905108 Sequence 905108,
c 22	13.8	69.0	24	12	US-11-137-315A-19 Sequence 19, Appl
c 23	13.8	69.0	25	12	US-11-121-849-429730 Sequence 429730,
c 24	13.8	69.0	25	12	US-11-121-849-431098 Sequence 431098,
c 25	13.8	69.0	25	12	US-11-121-849-431099 Sequence 431099,
c 26	13.8	69.0	25	12	US-11-121-849-515908 Sequence 515908,
c 27	13.8	69.0	25	12	US-11-121-849-673778 Sequence 673778,
c 28	13.8	69.0	25	12	US-11-121-849-673779 Sequence 673779,
c 29	13.6	68.0	25	12	US-11-136-527-309344 Sequence 309344,
c 30	13.6	68.0	25	12	US-11-136-527-309345 Sequence 309345,
c 31	13.6	68.0	25	12	US-11-136-527-309352 Sequence 309352,
c 32	13.6	68.0	25	12	US-11-136-527-309363 Sequence 309363,
c 33	13.6	68.0	25	12	US-11-136-527-309371 Sequence 309371,
c 34	13.6	68.0	25	12	US-11-136-527-309372 Sequence 309372,
c 35	13.4	67.0	19	10	US-11-101-244-1149636 Sequence 1149636,
c 36	13.4	67.0	19	11	US-11-083-784-1149636 Sequence 1149636,
c 37	13.4	67.0	23	8	US-10-310-914A-905217 Sequence 905217,
c 38	13.4	67.0	25	12	US-11-121-849-192 Sequence 192, App
c 39	13.4	67.0	25	12	US-11-121-849-118160 Sequence 118160,
c 40	13.4	67.0	25	12	US-11-121-849-206299 Sequence 206299,
c 41	13.4	67.0	25	12	US-11-121-849-206858 Sequence 206858,
c 42	13.4	67.0	25	12	US-11-121-849-208795 Sequence 208795,
c 43	13.4	67.0	25	12	US-11-121-849-257563 Sequence 257563,
c 44	13.4	67.0	25	12	US-11-121-849-285022 Sequence 285022,
c 45	13.4	67.0	25	12	US-11-121-849-322158 Sequence 322158,

ALIGNMENTS

RESULT 1

US-11-121-849-529681

; Sequence 529681, Application US/11121849

; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 529681

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-11-121-849-529681

Query Match 82.0%; Score 16.4; DB 12; Length 25;
Best Local Similarity 94.4%; Pred No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTTTCACCAATGGAAG 19

Db 1 CTTTCACCAATGGAAG 18

RESULT 2

US-11-121-849-447577/c

; Sequence 447577, Application US/11121849

; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

Query Match 75.0%; Score 15; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays


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RESULT 9
US-11-121-849-206856/c
; Sequence 206856, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 206856
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-206856

```

```

Query Match      71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 68.4%; Pred. NO. 1.2e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 CTTTCACCAAAATTGGAAGC 20
      |:|:|:|:|:|:|:|:|:|
DB      6 CUUCCACCCAGUGGAAGC 24

RESULT 12
US-11-121-849-191
; Sequence 191, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:

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/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ TITLE OF INVENTION: Microarrays
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 191
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-191

Query Match 71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATGGGAAGC 20
Db 4 CATGCACCTAATGGGAAGC 22

RESULT 13
US-11-121-849-345854
/ Sequence 345854, Application US/11/121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ TITLE OF INVENTION: Microarrays
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 345854
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-345854

Query Match 71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATGGGAAGC 20
Db 2 CCTTGACCAAAATGGGAAGC 20

RESULT 14
US-11-121-849-673774
/ Sequence 673774, Application US/11/121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ TITLE OF INVENTION: Microarrays
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 673774
/ LENGTH: 25
/ TYPE: DNA
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/ ORGANISM: Homo sapien
US-11-121-849-673774

Query Match 71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATGGGAAGC 20
Db 4 CATGCACCTAATGGGAAGC 22

RESULT 15
US-11-121-849-673775
/ Sequence 673775, Application US/11/121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ TITLE OF INVENTION: Microarrays
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 673775
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-673775

Query Match 71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATGGGAAGC 20
Db 3 CATGCACCTAATGGGAAGC 21

Search completed: March 4, 2006, 03:54:50
Job time : 497.289 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:49:48 ; Search time 417.368 Seconds
(without alignments)
396.263 Million cell updates/sec

Title: US-09-701-583A-14

Perfect score: 20
Sequence: 1 gctttcaccataattggaagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10900902

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	US-10-220-033-5
2	20	100.0	20	9	US-10-984-919-532
3	18	90.0	18	9	US-10-984-919-1273
4	18	90.0	20	6	US-10-189-267-36
5	18	90.0	20	6	US-10-189-267-182
6	16	80.0	16	9	US-10-984-919-1275
7	16	80.0	18	5	US-10-146-058-79
8	16	80.0	18	9	US-10-984-919-1215
9	15.8	79.0	25	10	US-11-036-317-862259
10	15.8	79.0	25	10	US-11-036-317-873649
11	15.8	79.0	25	10	US-11-036-317-940468
12	15.2	76.0	25	7	US-10-719-956-259831
13	15	75.0	15	9	US-10-984-919-1274
14	14.8	74.0	25	10	US-11-060-756-239401
15	14.4	72.0	25	8	US-10-719-900-974400
16	14.4	72.0	25	9	US-10-956-157-147123
17	14.4	72.0	25	10	US-11-036-317-915488
18	14.4	72.0	25	10	US-11-036-317-986433
19	14.2	71.0	20	3	US-09-922-549B-60
20	14.2	71.0	20	6	US-10-114-739A-60
21	14.2	71.0	25	7	US-10-681-773-64719
22	14.2	71.0	25	7	US-10-681-773-103539
23	14.2	71.0	25	7	US-10-719-956-585916

C 24	14.2	71.0	25	8	US-10-719-900-930639	Sequence 930639,
C 25	14.2	71.0	25	9	US-10-809-189-6827	Sequence 6827, Ap
C 26	14.2	71.0	25	10	US-11-036-317-862258	Sequence 862258,
C 27	14.2	71.0	25	10	US-11-036-317-873648	Sequence 873648,
C 28	14.2	71.0	25	10	US-11-036-317-940467	Sequence 940467,
C 29	14.2	71.0	25	10	US-11-060-756-63888	Sequence 63888, A
C 30	14.2	71.0	25	10	US-11-060-756-63903	Sequence 63903, A
C 31	14.2	71.0	25	10	US-11-060-756-260911	Sequence 260911,
C 32	14.2	71.0	25	10	US-11-060-756-262958	Sequence 262958,
C 33	14.2	71.0	25	10	US-11-060-756-277348	Sequence 277348,
C 34	14	70.0	25	7	US-10-719-956-313402	Sequence 313402,
C 35	13.8	69.0	17	3	US-09-776-474-972	Sequence 972, App
C 36	13.8	69.0	19	9	US-10-898-660-73	Sequence 73, Appl
C 37	13.8	69.0	19	9	US-10-898-660-185	Sequence 185, App
C 38	13.8	69.0	25	7	US-10-719-956-121933	Sequence 121933,
C 39	13.8	69.0	25	7	US-10-719-956-612371	Sequence 612371,
C 40	13.8	69.0	25	7	US-10-719-956-623123	Sequence 623123,
C 41	13.8	69.0	25	8	US-10-719-900-379911	Sequence 379911,
C 42	13.8	69.0	25	8	US-10-719-900-415013	Sequence 415013,
C 43	13.8	69.0	25	8	US-10-719-900-492824	Sequence 492824,
C 44	13.8	69.0	25	9	US-10-956-157-131171	Sequence 131171,
C 45	13.8	69.0	25	10	US-11-036-317-789786	Sequence 789786,

ALIGNMENTS

RESULT 1
US-10-220-033-5
; Sequence 5, Application US/10220033
; Publication No. US20030186906A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsenstepen, Karl-Hermann
; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
; TITLE OF INVENTION: and a molecule binding to an expression product of that
; TITLE OF INVENTION: gene
; FILE REFERENCE: P68119US0
; CURRENT APPLICATION NUMBER: US/10/220,033
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: PCT/EP01/02694
; PRIOR FILING DATE: 2001-03-10
; PRIOR APPLICATION NUMBER: EP00105190.3
; PRIOR FILING DATE: 2000-03-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide
US-10-220-033-5

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTTCACCAATTCGAAGC 20
|||||
DB 1 GCTTTCACCAATTCGAAGC 20

RESULT 2
US-10-984-919-532
; Sequence 532, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsenstepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763US0

; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 532
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-532

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATTGGAAGC 20
|||||
Db 1 GCTTCCACCAAAATTGGAAGC 20

RESULT 3
US-10-984-919-1273
; Sequence 1273, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1273
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1273

Query Match 90.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGAAG 19
|||||
Db 1 CTTTCACCAAAATTGGAAG 18

RESULT 4
US-10-189-267-36
; Sequence 36, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-36

Query Match 90.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATTGGA 18
|||||
Db 3 GCTTCCACCAAAATTGGA 20

RESULT 5
US-10-189-267-182/c
; Sequence 182, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 182
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-182

Query Match 90.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCCACCAAAATTGGA 18
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Db 18 GCTTCCACCAAAATTGGA 1

RESULT 6
US-10-984-919-1275
; Sequence 1275, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1275
; LENGTH: 16
; TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1275

Query Match 80.0%; Score 16; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCACCAAAATTGGAAGC 20

Db 1 TCACCAAAATTGGAAGC 16

RESULT 7

US-10-146-058-79
; Sequence 79, Application US/10146058
; Publication No. US20030040499A1

GENERAL INFORMATION:

APPLICANT: Schlengersiepen, Georg-Ferdinand

APPLICANT: Brysch, Wolfgang

APPLICANT: Schlengersiepen, Karl-Hermann

APPLICANT: Schlengersiepen, Reimar

APPLICANT: Bogdahn, Ulrich

TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

NUMBER OF SEQUENCES: 137

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern

STREET: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/146,058

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/535,249

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93 107 089.0

FILING DATE: 30-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93 107 849.7

FILING DATE: 13-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.

REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10577/P59418

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666

TELEFAX: (202) 393-5350

TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: YES

US-10-146-058-79

Query Match 80.0%; Score 16; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCACCAAAATTGGAAGC 20

Db 1 TCACCAAAATTGGAAGC 16

RESULT 8

US-10-984-919-1215

; Sequence 1215, Application US/10984919

; Publication No. US20050130927A1

GENERAL INFORMATION:

APPLICANT: Schlengersiepen, Karl-Hermann

APPLICANT: Brysch, Wolfgang

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

FILE REFERENCE: 10496/P63763USO

CURRENT APPLICATION NUMBER: US/10/984,919

CURRENT FILING DATE: 2004-11-10

PRIOR APPLICATION NUMBER: US/09/341,700

PRIOR FILING DATE: 1999-09-24

PRIOR APPLICATION NUMBER: PCT/EP98/00497

PRIOR FILING DATE: 1998-01-30

PRIOR APPLICATION NUMBER: EP 97 101 531.8

PRIOR FILING DATE: 1997-01-31

NUMBER OF SEQ ID NOS: 1764

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 1215

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: antisense oligonucleotide

US-10-984-919-1215

Query Match 80.0%; Score 16; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCACCAAAATTGGAAGC 20

Db 1 TCACCAAAATTGGAAGC 16

RESULT 9

US-11-036-317-862259/c

; Sequence 862259, Application US/11036317

; Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 862259

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-862259

Query Match 79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTTTCACCAAAATTGGAAGC 20

Db 22 CTTTCACCAAAAGTGAGGC 4

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RESULT 10
US-11-036-317-873649/c
; Sequence 873649, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 873649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-873649

Query Match          79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CTTTCACCAAAATTTGGAAGC 20
Db      20  CTTTCACCAAAATTTGGAAGC 2

RESULT 11
US-11-036-317-940468/c
; Sequence 940468, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 940468
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-940468

Query Match          79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CTTTCACCAAAATTTGGAAGC 20
Db      19  CTTTCACCAAAATTTGGAAGC 1

RESULT 12
US-10-719-956-259831/c
; Sequence 259831, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,936
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 259831
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-259831

Query Match          76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCTTTACCAAAATTTGGAAGC 20
Db      23  GCTGTACGACAAATTTGAAGC 4

RESULT 13
US-10-984-919-1274
; Sequence 1274, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1274

Query Match          75.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  CACCAAAATTTGGAAGC 20
Db      1  CACCAAAATTTGGAAGC 15

RESULT 14
US-11-060-756-239401
; Sequence 239401, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239401
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-239401
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Query Match 74.0%; Score 14.8; DB 10; Length 25;
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTTCACCAAAATTGGAAG 19
 |||||
 DB 3 CTTTCACCAAAATTGAGG 20

RESULT 15
 US-10-719-900-974400/c
 ; Sequence 974400, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 974400
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-974400

Query Match 72.0%; Score 14.4; DB 8; Length 25;
 Best Local Similarity 93.8%; Pred. No. 3e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TCACCAAAATTGGAAGC 20
 |||||
 DB 19 TCACCAAAAGTGAAGC 4

Search completed: March 4, 2006, 07:04:14
 Job time : 419.368 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2006, 01:42:16 ; Search time 861.632 Seconds
(without alignments)
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Title: US-09-701-583A-9

Perfect score: 18
Sequence: 1 cggcatgtctatttga 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1934910

Minimum DB seq length: 0
Maximum DB seq length: 409

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6 A40535	A40535 Sequence 72
2	18	100.0	18	6 A89061	A89061 Sequence 12
3	18	100.0	18	6 BD066574	BD066574 An antise
4	18	100.0	18	6 BD234905	BD234905 A method
5	18	100.0	18	6 CS123678	CS123678 Sequence
6	18	100.0	18	6 AR232815	AR232815 Sequence
7	18	100.0	18	6 AX008976	AX008976 Sequence
8	18	100.0	18	6 AX030110	AX030110 Sequence
9	18	100.0	18	6 AX252494	AX252494 Sequence
10	18	100.0	18	6 AX316431	AX316431 Sequence
11	18	100.0	22	6 BD234967	BD234967 A method
12	18	100.0	22	6 AX009038	AX009038 Sequence
13	18	100.0	27	6 AX113805	AX113805 Sequence
14	16	88.9	16	6 A89129	A89129 Sequence 12
15	16	88.9	16	6 BD066642	BD066642 An antise
16	16	88.9	16	6 BD234928	BD234928 A method
17	16	88.9	16	6 AX008999	AX008999 Sequence
18	16	88.9	20	6 A88381	A88381 Sequence 52

19	16	88.9	20	6 A90348	A90348 Sequence 52
20	16	88.9	20	6 BD065894	BD065894 An antise
21	16	88.9	20	6 BD234904	BD234904 A method
22	16	88.9	20	6 BD234965	BD234965 A method
23	16	88.9	20	6 CS123678	CS123678 Sequence
24	16	88.9	20	6 AX008975	AX008975 Sequence
25	16	88.9	20	6 AX009036	AX009036 Sequence
26	14.4	80.0	17	6 BD203421	BD203421 Method an
27	14	77.8	17	6 BD203422	BD203422 Method an
28	13.8	76.7	20	6 AR130778	AR130778 Sequence
c 29	13.4	74.4	30	6 CS130581	CS130581 Sequence
c 30	13	72.2	17	6 BD203423	BD203423 Method an
c 31	12.8	71.1	22	6 AR393715	AR393715 Sequence
32	12.4	68.9	20	6 AR647382	AR647382 Sequence
33	12.4	68.9	20	6 AR654435	AR654435 Sequence
c 34	12.4	68.9	24	6 AR321595	AR321595 Sequence
35	12.4	68.9	38	6 A35024	A35024 Synthetic P
c 36	12.2	67.8	18	6 AR299597	AR299597 Sequence
c 37	12.2	67.8	23	6 BD184058	BD184058 Method an
c 38	12.2	67.8	23	6 AX742234	AX742234 Sequence
c 39	12.2	67.8	23	6 AX798838	AX798838 Sequence
c 40	12.2	67.8	24	6 AR075414	AR075414 Sequence
c 41	12.2	67.8	24	6 BD176117	BD176117 Anticoagu
42	12.2	67.8	25	6 CO986684	CO986684 Sequence
43	12.2	67.8	25	6 AR455613	AR455613 Sequence
44	12.2	67.8	25	6 AX353402	AX353402 Sequence
45	12.2	67.8	28	10 AL773120	AL773120 Arabidops

ALIGNMENTS

RESULT 1
A40535
LOCUS A40535 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 72 from Patent WO9425578.
ACCESSION A40535
VERSION A40535.1 GI:2296570
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE unclassified sequences.
AUTHORS 1 (bases 1 to 18)
TITLE
JOURNAL
FEATURES
source
location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
Patent: WO 9425578-A 72 10-NOV-1994;
BIOGNOSTIK GES (DE)

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCATGCTATTGTGA 18
|||||
DB 1 CGGCATGCTATTGTGA 18
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RESULT 2

A89061
LOCUS A89061 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1209 from Patent WO9833904.
ACCESSION A89061
VERSION A89061.1 GI:6737631
KEYWORDS
SOURCE unidentified
ORGANISM unclassified

AR232815 LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 72 from patent US 6455689.
ACCESSION AR232815
VERSION AR232815.1 GI:27275153
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 72 24-SEP-2002;
Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH;
Gottengen;
EPX; Location/Qualifiers
FEATURES
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCATGCTCTATTGTGA 18
|||||
Db 1 CGGCATGCTCTATTGTGA 18
RESULT 7
LOCUS AX008976 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 9 from Patent WO9963975.
ACCESSION AX008976
VERSION AX008976.1 GI:9996350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 9 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCATGCTCTATTGTGA 18
|||||
Db 1 CGGCATGCTCTATTGTGA 18
RESULT 8
LOCUS AX030110 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 72 from Patent EP1008649.
ACCESSION AX030110
VERSION AX030110.1 GI:10190327

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 72 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
source 1..18
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCATGCTCTATTGTGA 18
|||||
Db 1 CGGCATGCTCTATTGTGA 18
RESULT 9
LOCUS AX252494 18 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 4 from Patent WO0168146.
ACCESSION AX252494
VERSION AX252494.1 GI:15985765
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE Mixture comprising an inhibitor or suppressor of a gene and a
molecule binding to an expression product of that gene
JOURNAL Patent: WO 0168146-A 4 20-SEP-2001;
Biognostik Gesellschaft fuer biomolekulare Diagnostik mbH (DE)
FEATURES
source 1..18
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCATGCTCTATTGTGA 18
|||||
Db 1 CGGCATGCTCTATTGTGA 18
RESULT 10
LOCUS AX316431 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 72 from Patent EP1160319.
ACCESSION AX316431
VERSION AX316431.1 GI:17899604
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
sequences.

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REFERENCE
1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 72 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
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/note="Description of unknown: unknown"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCATGCTCTATTGTGA 18
|||||
Db 1 CGGCATGCTCTATTGTGA 18
|||||

RESULT 11
BD234967 22 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234967
VERSION BD234967.1 GI:33044737
KEYWORDS JP 2002517434-A/71.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 22)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 71 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/71
PD 18-JUN-2002
PP 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG RI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
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QY 1 CGGCATGCTCTATTGTGA 18
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Db 5 CGGCATGCTCTATTGTGA 22
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REFERENCE
1
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 71 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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Db 5 CGGCATGCTCTATTGTGA 22
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RESULT 13
AX113805 27 bp DNA linear PAT 01-MAY-2001
LOCUS
DEFINITION Sequence 51 from Patent WO0127256.
ACCESSION AX113805
VERSION AX113805.1 GI:13939971
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE Wu,L., Carey,M.P. and Belldgrun,A.S.
AUTHORS Chimeric transcriptional regulatory element and methods for
TITLE prostate-targeted gene expression
JOURNAL Patent: WO 0127256-A 51 19-APR-2001;
The Regents of the University of California System (US)
FEATURES
source Location/Qualifiers
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RESULT 14
A89129 16 bp DNA linear PAT 23-JAN-2000
LOCUS
DEFINITION Sequence 1277 from Patent WO9833904.
ACCESSION A89129
VERSION A89129.1 GI:6737699
KEYWORDS unidentified
SOURCE
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LOCUS
AX009038 22 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 71 from Patent WO9963975.
ACCESSION AX009038
VERSION AX009038.1 GI:9996412
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
AUTHORS A method for stimulating the immune system
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 71 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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Db 5 CGGCATGCTCTATTGTGA 22
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RESULT 13
AX113805 27 bp DNA linear PAT 01-MAY-2001
LOCUS
DEFINITION Sequence 51 from Patent WO0127256.
ACCESSION AX113805
VERSION AX113805.1 GI:13939971
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE Wu,L., Carey,M.P. and Belldgrun,A.S.
AUTHORS Chimeric transcriptional regulatory element and methods for
TITLE prostate-targeted gene expression
JOURNAL Patent: WO 0127256-A 51 19-APR-2001;
The Regents of the University of California System (US)
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/note="SYNTHETIC OLIGONUCLEOTIDE"
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 CGGCATGCTCTATTGTGA 20
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RESULT 14
A89129 16 bp DNA linear PAT 23-JAN-2000
LOCUS
DEFINITION Sequence 1277 from Patent WO9833904.
ACCESSION A89129
VERSION A89129.1 GI:6737699
KEYWORDS unidentified
SOURCE
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ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1277 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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/db_xref="taxon:32644"

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCATGCTCTATTG 16
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DB 1 CGGCATGCTCTATTG 16

RESULT 15
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LOCUS 16 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066642
VERSION BD066642.1 GI:22612245
KEYWORDS JP 2001511000-A/1277.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1277 07-AUG-2001;
BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/1277
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
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FEATURES
source

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
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QY 1 CGGCATGCTCTATTG 16
|||||
DB 1 CGGCATGCTCTATTG 16

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Job time : 862.632 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using bw model

Run on: March 4, 2006, 01:49:32 ; Search time 69.1579 Seconds
(without alignments)
462.653 Million cell updates/sec

Title: US-09-701-583A-9

Perfect score: 18
Sequence: 1 cgcgcgtctctcttgc 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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Listing first 45 summaries

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SUMMARIES

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1	18	100.0	18	3	US-08-535-249-72
2	13.8	76.7	20	3	US-09-429-322-29
3	13.4	74.4	20	3	US-10-053-662A-7
4	13.2	73.3	25	3	US-09-396-196G-19083
5	13.2	72.3	25	3	US-09-396-196G-72258
6	12.8	71.1	22	3	US-09-526-193A-254
7	12.4	68.9	20	3	US-10-393-905-35
8	12.4	68.9	20	3	US-10-660-253-21
9	12.4	68.9	24	3	US-09-460-555-3
10	12.2	67.8	24	3	US-09-422-978-11332
11	12.2	67.8	24	2	US-08-273-402B-9
12	12.2	67.8	25	3	US-09-903-013-11
13	12.2	67.8	31	2	US-08-823-516-113
14	12.2	67.8	31	3	US-08-759-038-134
15	12.2	67.8	31	3	US-08-758-314-134
16	12.2	67.8	31	3	US-09-684-938-134
17	12.2	67.8	31	3	US-09-308-825A-134
18	12.2	67.8	31	3	US-09-940-244-113
19	12.2	67.8	31	3	US-09-381-212-113
20	12.2	67.8	31	3	US-09-713-601A-113
21	12	66.7	27	3	US-09-964-994B-3
22	11.8	65.6	30	2	US-08-479-487-65
23	11.8	65.6	15	2	US-08-311-486C-105
24	11.8	65.6	15	2	US-08-311-486C-631

25	11.8	65.6	15	9	5182195-62	Patent No. 5182195
26	11.8	65.6	19	3	US-09-475-947A-61	Sequence 61, Appl
27	11.8	65.6	20	2	US-08-599-252-2	Sequence 2, Appl
28	11.8	65.6	20	2	US-08-436-074-2	Sequence 2, Appl
29	11.8	65.6	20	3	US-09-166-186-88	Sequence 88, Appl
30	11.8	65.6	20	3	US-09-166-186-132	Sequence 132, App
31	11.8	65.6	20	3	US-09-313-932-88	Sequence 88, Appl
32	11.8	65.6	20	3	US-09-313-932-132	Sequence 132, App
33	11.8	65.6	20	3	US-09-313-932-453	Sequence 453, App
34	11.8	65.6	20	3	US-09-887-145-43	Sequence 43, Appl
35	11.8	65.6	20	6	PCT-US96-06352-2	Sequence 2, Appl
36	11.8	65.6	20	6	PCT-US96-06583-2	Sequence 2, Appl
37	11.8	65.6	21	3	US-09-422-978-10510	Sequence 10510, A
38	11.8	65.6	21	3	US-09-382-552-124	Sequence 124, App
39	11.8	65.6	22	2	US-08-217-529-6	Sequence 6, Appl
40	11.8	65.6	23	6	PCT-US93-02259-13	Sequence 13, Appl
41	11.8	65.6	25	3	US-09-336-196G-118255	Sequence 118255,
42	11.8	65.6	25	3	US-09-336-196G-118256	Sequence 118256,
43	11.8	65.6	25	3	US-09-396-196G-118257	Sequence 118257,
44	11.8	65.6	26	3	US-09-077-734-40	Sequence 40, Appl
45	11.8	65.6	30	3	US-09-276-147B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-535-249-72
; Sequence 72, Application US/08535249
; Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESSES:
ADDRESS: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202)393-5350
TELEX: RCA 248593 IDBA UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-72

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGGCATGCTATTGTA 18

RESULT 2
US-09-429-322-29
Sequence 29, Application US/09429322A
Patent No. 6190869

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Coweest

TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN KINASE C-THETA

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: RTS-0100

CURRENT APPLICATION NUMBER: US/09/429,322A

CURRENT FILING DATE: 1999-10-26

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 29

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Antisense Oligonucleotide

US-09-429-322-29

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Best Local Similarity 88.2%; Pred. No. 9.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCATGCTATTGTA 18
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DB 2 GGCATGCTATTGTA 18

RESULT 3
US-10-053-662A-7
Sequence 7, Application US/10053662A
Patent No. 6916618

GENERAL INFORMATION:

APPLICANT: Alexandra Charlesworth

APPLICANT: Falvia Spilito

APPLICANT: Guerrino Meneguzzi

APPLICANT: John Baird

TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN

TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS

FILE REFERENCE: P84us4

CURRENT APPLICATION NUMBER: US/10/053,662A

CURRENT FILING DATE: 2002-01-24

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: primer

US-10-053-662A-7

QY 4 CATGCTATTGTA 18
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DB 1 CCTGCTATTGTA 15

RESULT 4
US-09-396-196G-19083
Sequence 19083, Application US/09396196G
Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 19083

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-09-396-196G-19083

Query Match 73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGCATGCTATTGTA 18
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DB 8 CAGCATGCTATTGTA 25

RESULT 5
US-09-396-196G-72258/c
Sequence 72258, Application US/09396196G
Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 72258

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-72258

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Best Local Similarity 83.3%; Pred. No. 2e+03;
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QY 1 CGGCATGCTATTGTA 18
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DB 20 CGGCATGCTATTGTA 3

RESULT 6
US-09-526-193A-254/c
Sequence 254, Application US/09526193A


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Patent No. 6617122
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pimstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; FILE OF INVENTION: CHOLESTEROL LEVELS
; FILE REFERENCE: 50110/002005
; CURRENT APPLICATION NUMBER: US/09/526,193A
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-254

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DB      21 GCATTTCTATTTTGA 6

RESULT 7
US-10-393-905-35
; Sequence 35, Application US/10393905
; GENERAL INFORMATION:
; APPLICANT: OETTGEN, PETER
; APPLICANT: LIBERMANN, TOMIA
; APPLICANT: GOLDRING, MARY
; TITLE OF INVENTION: USE OF TRANSCRIPTION FACTORS FOR TREATING INFLAMMATION
; FILE REFERENCE: 49923CIP (72037)
; CURRENT APPLICATION NUMBER: US/10/393,905
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: PCT/US01/29340
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,379
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-393-905-35

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Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CATGCTATTTTGT 17
DB      2 CATGCTTTTGT 15

RESULT 8
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US-10-660-253-21
; Sequence 21, Application US/10660253
; Patent No. 6889143
; GENERAL INFORMATION:
; APPLICANT: Benlike, Mark A.
; APPLICANT: Lingyan, Huang
; APPLICANT: Owczarzy, Richard
; APPLICANT: Walder, Joseph A.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR ESTIMATING THE MELTING TEMPERATURE (Tm) F
; FILE REFERENCE: 03988/100K297-US1
; CURRENT APPLICATION NUMBER: US/10/660,253
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/410,663
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-660-253-21

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Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 ATGCTATTTTGTGA 18
DB      2 ATGTATATTTTGA 15

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US-09-460-555-3/c
; Sequence 3, Application US/09460555
; Patent No. 6563014
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: Goldstein, Harris
; APPLICANT: Paul, Jesse B.
; TITLE OF INVENTION: SELF-CONTAINED SYSTEM FOR SUSTAINED VIRAL REPLICATION
; FILE REFERENCE: 96700/552
; CURRENT APPLICATION NUMBER: US/09/460,555
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-460-555-3

Query Match      68.9%; Score 12.4; DB 3; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 ATGCTATTTTGTGA 18
DB      20 ATGCTATTTTGA 7

RESULT 10
US-09-422-978-11332/c
; Sequence 11332, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
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;; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;; FILE REFERENCE: GENSET.020CPI
;; CURRENT APPLICATION NUMBER: US/09/422,978
;; CURRENT FILING DATE: 1999-10-20
;; EARLIER APPLICATION NUMBER: US 09/298,850
;; EARLIER FILING DATE: 1999-04-21
;; EARLIER APPLICATION NUMBER: US 60/109,732
;; EARLIER FILING DATE: 1998-11-23
;; EARLIER APPLICATION NUMBER: US 60/082,614
;; EARLIER FILING DATE: 1998-04-21
;; NUMBER OF SEQ ID NOS: 11796
;; SEQ ID NO: 11332
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: primer_bind
;; LOCATION: 1..18
;; OTHER INFORMATION: downstream amplification primer 99-4284 for SEQ 3467, in compleme
US-09-422-978-11332

Query Match 67.8%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCACTCTATTGTGA 18
DB 18 GGCAGCTCTACTTTGCA 2

RESULT 11
US-08-273-402B-9
; Sequence 9, Application US/08273402B
; Patent No. 5958403
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry
; APPLICANT: Rubin-Kelly, Vicki E.
; APPLICANT: Lieberman, Towia
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR
; TITLE OF INVENTION: PREVENTION OF GRAFT REJECTION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,402B
; FILING DATE: 11-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,569
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/843,731
; FILING DATE: 28-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 05311/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 24
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-273-402B-9

Query Match 67.8%; Score 12.2; DB 2; Length 24;
Best Local Similarity 82.4%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCACTCTATTGTGA 18
DB 1 GGCAGCTCTACTTTGGA 17

RESULT 12
US-09-903-013-11
; Sequence 11, Application US/09903013
; Patent No. 6685950
; GENERAL INFORMATION:
; APPLICANT: Weber, Olaf
; APPLICANT: Schlapp, Tobias
; APPLICANT: Siegling, Angela
; APPLICANT: Knorr, Andreas
; APPLICANT: Hirth-Dietrich, Claudia
; APPLICANT: Theiss, Gudrun
; TITLE OF INVENTION: Use of Strains of Parapoxvirus Ovis for Producing Antiviral Medic
; TITLE OF INVENTION: and Medicaments Against Cancer
; FILE REFERENCE:lea 34 376
; CURRENT APPLICATION NUMBER: US/09/903,013
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: DE10033582.9
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: DE10122451.6
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-903-013-11

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCACTCTATTGTGA 18
DB 1 GGCAGCTCTACTTTGGA 17

RESULT 13
US-08-823-516-113/c
; Sequence 113, Application US/08823516
; Patent No. 5994069
; GENERAL INFORMATION:
; APPLICANT: Hall, Jeff G.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Mast, Andrea L.
; APPLICANT: Brow, Mary Ann D.
; TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
; TITLE OF INVENTION: Sequential Invasive Cleavages
; NUMBER OF SEQUENCES: 163
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(1..2, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(3, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(4..5, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(6..8, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(9, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(10, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
US-08-823-516-113

Query Match 67.8%; Score 12.2; DB 2; Length 31;

Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY 2 GGCATGCTATTGTGA 18
DB 31 GGCCTGTTATTGTGA 15
RESULT 14
US-08-759-038-134/C
Sequence 134, Application US/08759038
Patent No. 6090543
GENERAL INFORMATION:
APPLICANT: Prudent, James R.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamatchev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Dahlberg, James E.
TITLE OF INVENTION: Cleavage Of Nucleic Acids
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,038
FILING DATE: 02-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02574
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(1..2, "")
OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(3, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
FEATURE:
NAME/KEY: misc difference
LOCATION: replace(4..5, "")

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/ OTHER INFORMATION: /note="The residues at these
/ OTHER INFORMATION: positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(6..8, "")
/ OTHER INFORMATION: /note="The residues at these
/ OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate).
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(9, "")
/ OTHER INFORMATION: /note="The residue at this
/ OTHER INFORMATION: position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(10, "")
/ OTHER INFORMATION: /note="The residue at this
/ OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
/ US-08-759-038-134

Query Match 67.8%; Score 12.2; DB 3; Length 31;
Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGCGTGTATTGTGA 18
Db 31 GGCGTGTATTGTGA 15

RESULT 15
US-08-758-314-134/C
Sequence 134, Application US/08758314
Patent No. 6090606
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Improved Cleavage Agents
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,314
FILING DATE: 02-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
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/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(1..2, "")
/ OTHER INFORMATION: /note="The residues at these
/ OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(3, "")
/ OTHER INFORMATION: /note="The residue at this
/ OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(4..5, "")
/ OTHER INFORMATION: /note="The residues at these
/ OTHER INFORMATION: positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)."
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(6..8, "")
/ OTHER INFORMATION: /note="The residues at these
/ OTHER INFORMATION: positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(9, "")
/ OTHER INFORMATION: /note="The residue at this
/ OTHER INFORMATION: position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)."
/ FEATURE:
/ NAME/KEY: misc_difference
/ LOCATION: replace(10, "")
/ OTHER INFORMATION: /note="The residue at this
/ OTHER INFORMATION: position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
/ US-08-758-314-134

Query Match 67.8%; Score 12.2; DB 3; Length 31;
Best Local Similarity 82.4%; Pred. No. 6.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGCGTGTATTGTGA 18
Db 31 GGCGTGTATTGTGA 15
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Search completed: March 4, 2006, 02:07:27
Job time : 70.1579 secs